IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

In re the application of: Markus Pompejus *et al.*	**Group Art Unit:** Not Yet Assigned
Serial No.: Not Yet Assigned	**Examiner:** Not Yet Assigned
Filed: Herewith	
For: *"Corynebacterium Glutamicum Genes Encoding Metabolic Pathway Proteins"*	
Attorney Docket No.: BGI-121CP2	

Assistant Commissioner for Patents
BOX SEQUENCE LISTING
Washington, DC 20231

TRANSMITTAL LETTER FOR DISKETTE OF SEQUENCE LISTING

Dear Sir:

Enclosed is a diskette which contains a computer readable form of the Sequence Listing for the patent application filed herewith. The Sequence Listing complies with the requirements of 37 C.F.R. §1.821. The material on this disk is identical in substance to the paper copy of the Sequence Listing appearing on pages 1 - 175, which is submitted herewith, as required by 37 CFR §1.821(f). The computer readable form of the Sequence Listing contained on the enclosed disk is understood to comply with the requirements of §1.824(d).

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Signature [signature]

Larry Taylor
Please Print Name of Person Signing

LAHIVE & COCKFIELD, LLP

Attorneys at Law

By: [signature]

Elizabeth A. Hanley
Registration No. 33,505
28 State Street
Boston, MA 02109

Date: **December 22, 2000**

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SEQUENCE LISTING

<110> Pompejus, Markus
Kroger, Burkhard
Schroder, Hartwig
Zelder, Oskar
Haberhauer, Gregor
Kim, Jun-Won
Lee, Heung-Schick
Hwang, Byung-Joon

<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING METABOLIC PATHWAY PROTEINS

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Gly Glu Thr Phe Ala Asn Pro Gln Ala Asp Val Leu Asp Ile Pro Ala
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Thr Ile Ala Thr Ala Ala Leu Val Arg Pro Leu Glu Leu Gly Ala Asp
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ttg cct gca tac cct cct ttc att gag ttg cct aag gtg act ggt cgt    535
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Gln Ala Ile Tyr Ile Asp Ala His Glu Tyr Asp Leu Lys Glu Ile Glu
     85                  90                  95

aag gcc ttc gct gac ggt gcg gga tca ctg ttg ttc tgc aat cca cac    631
Lys Ala Phe Ala Asp Gly Ala Gly Ser Leu Leu Phe Cys Asn Pro His
100                 105                 110                 115

aac cca ctg ggc acg gtc ttt tct gaa gag tac atc cgc gag ctc acc    679
Asn Pro Leu Gly Thr Val Phe Ser Glu Glu Tyr Ile Arg Glu Leu Thr
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        150                 155                 160

gag aac gct gca aac act tgc atc acc atc acc gca act tct aag gcg    823
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Val Ser Ile Leu Gly Leu Ile Ala Ala Glu Thr Val Tyr Asn Glu Gly
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Glu Glu Phe Leu Asp Glu Ser Ile Gln Ile Leu Lys Asp Asn Arg Asp
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    130                 135                 140

Glu Ile His Ala Pro Leu Val Tyr Glu Gly Thr His Val Val Ala Ala
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Gly Val Ser Glu Asn Ala Ala Asn Thr Cys Ile Thr Ile Thr Ala Thr
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Ser Lys Ala Trp Asn Thr Ala Gly Leu Lys Cys Ala Gln Ile Phe Phe
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Ser Asn Glu Ala Asp Val Lys Ala Trp Lys Asn Leu Ser Asp Ile Thr
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Arg Asp Gly Val Ser Ile Leu Gly Leu Ile Ala Ala Glu Thr Val Tyr
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Asn Glu Gly Glu Glu Phe Leu Asp Glu Ser Ile Gln Ile Leu Lys Asp
225                 230                 235                 240

Asn Arg Asp Phe Ala Ala Ala Glu Leu Glu Lys Leu Gly Val Lys Val
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Tyr Ala Pro Asp Ser Thr Tyr Leu Met Trp Leu Asp Phe Ala Gly Thr
            260                 265                 270

Lys Ile Glu Glu Ala Pro Ser Lys Ile Leu Arg Glu Glu Gly Lys Val
        275                 280                 285

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 70                  75                  80                  85

atc ggg cac acc atc gct gaa ggc agt ccc atc gac atg ctg ttg gaa    403
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ggc gcc gaa ctc gtt gca gtt cac acc tgg atg gac atg cag gta cag    691
Gly Ala Glu Leu Val Ala Val His Thr Trp Met Asp Met Gln Val Gln
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gca tca ctt gca ggt ctt gca gct gct caa cag cag tgg gat gaa gtg    739
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aagccttgga gattttgggt ctacaatagc gagggtgaat ttg acc atc ccc ttt   115
                                              Leu Thr Ile Pro Phe
                                                1               5

gcc aaa ggc cac gcc acc gaa aac gac ttc atc atc atc ccc gat gag   163
Ala Lys Gly His Ala Thr Glu Asn Asp Phe Ile Ile Ile Pro Asp Glu
                10                  15                  20

gat gcg cgc cta gat tta act cca gaa atg gtg gtc acg ctg tgt gac   211
Asp Ala Arg Leu Asp Leu Thr Pro Glu Met Val Val Thr Leu Cys Asp
            25                  30                  35

cgc cgc gcc ggg atc ggt gct gat ggt atc ctc cgc gtg gtt aaa gct   259
Arg Arg Ala Gly Ile Gly Ala Asp Gly Ile Leu Arg Val Val Lys Ala
        40                  45                  50

gca gac gta gaa ggc tcc acg gtc gac cca tcg ctg tgg ttc atg gat   307
Ala Asp Val Glu Gly Ser Thr Val Asp Pro Ser Leu Trp Phe Met Asp
    55                  60                  65

tac cgc aac gcc gat gga tct ttg gct gaa atg tgc ggc aat ggt gtg   355
Tyr Arg Asn Ala Asp Gly Ser Leu Ala Glu Met Cys Gly Asn Gly Val
70                  75                  80                  85

cgc ctg ttc gcg cac tgg ctg tac tcc cgc ggt ctt gtt gat aat acg   403
Arg Leu Phe Ala His Trp Leu Tyr Ser Arg Gly Leu Val Asp Asn Thr
                90                  95                  100

agc ttt gat atc ggt acc cgc gcc ggt gtc cgc cac gtt gat att ttg   451
Ser Phe Asp Ile Gly Thr Arg Ala Gly Val Arg His Val Asp Ile Leu
            105                 110                 115

cag gca gat caa cat tct gcg cag gtc cgc gtt gat atg ggc atc cct   499
Gln Ala Asp Gln His Ser Ala Gln Val Arg Val Asp Met Gly Ile Pro
        120                 125                 130

gac gtc acg gga tta tcc acc tgc gac atc aac ggc caa gta ttc gct   547
Asp Val Thr Gly Leu Ser Thr Cys Asp Ile Asn Gly Gln Val Phe Ala
    135                 140                 145
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ggc ctt ggc gtt gat atg ggt aac cca cac cta gcg tgc gtt gtg ccg 595
Gly Leu Gly Val Asp Met Gly Asn Pro His Leu Ala Cys Val Val Pro
150 155 160 165

ggc tta agt gcg tcg gct ctt gcc gat atg gaa ctg cgc gca cct acg 643
Gly Leu Ser Ala Ser Ala Leu Ala Asp Met Glu Leu Arg Ala Pro Thr
170 175 180

ttt gat cag gaa ttc ttc ccc cac ggt gtg aac gta gaa atc gtc aca 691
Phe Asp Gln Glu Phe Phe Pro His Gly Val Asn Val Glu Ile Val Thr
185 190 195

gaa tta gaa gat gac gca gta tcg atg cgc gtg tgg gaa cgc gga gtg 739
Glu Leu Glu Asp Asp Ala Val Ser Met Arg Val Trp Glu Arg Gly Val
200 205 210

ggc gaa acc cgc tcc tgt ggc acg gga acc gtt gct gca gcg tgt gct 787
Gly Glu Thr Arg Ser Cys Gly Thr Gly Thr Val Ala Ala Ala Cys Ala
215 220 225

gct tta gct gat gct gga ttg gga gaa ggc aca gct aaa gtg tgc gtt 835
Ala Leu Ala Asp Ala Gly Leu Gly Glu Gly Thr Ala Lys Val Cys Val
230 235 240 245

cca cgt ggg gaa gta gaa gtc cag atc ttt gac gac ggc tcc aca ctc 883
Pro Arg Gly Glu Val Glu Val Gln Ile Phe Asp Asp Gly Ser Thr Leu
250 255 260

acc ggc cca agc gcc atc atc gca ctc ggt gag gtg cag atc 925
Thr Gly Pro Ser Ala Ile Ile Ala Leu Gly Glu Val Gln Ile
265 270 275

taagattcgc gattgtagtt cgg 948

<210> 8
<211> 275
<212> PRT
<213> Corynebacterium glutamicum

<400> 8
Leu Thr Ile Pro Phe Ala Lys Gly His Ala Thr Glu Asn Asp Phe Ile
1 5 10 15

Ile Ile Pro Asp Glu Asp Ala Arg Leu Asp Leu Thr Pro Glu Met Val
20 25 30

Val Thr Leu Cys Asp Arg Arg Ala Gly Ile Gly Ala Asp Gly Ile Leu
35 40 45

Arg Val Val Lys Ala Ala Asp Val Glu Gly Ser Thr Val Asp Pro Ser
50 55 60

Leu Trp Phe Met Asp Tyr Arg Asn Ala Asp Gly Ser Leu Ala Glu Met
65 70 75 80

Cys Gly Asn Gly Val Arg Leu Phe Ala His Trp Leu Tyr Ser Arg Gly
85 90 95

Leu Val Asp Asn Thr Ser Phe Asp Ile Gly Thr Arg Ala Gly Val Arg
100 105 110

His Val Asp Ile Leu Gln Ala Asp Gln His Ser Ala Gln Val Arg Val
115 120 125

Asp Met Gly Ile Pro Asp Val Thr Gly Leu Ser Thr Cys Asp Ile Asn
130 135 140

Gly Gln Val Phe Ala Gly Leu Gly Val Asp Met Gly Asn Pro His Leu
145 150 155 160

Ala Cys Val Val Pro Gly Leu Ser Ala Ser Ala Leu Ala Asp Met Glu
165 170 175

Leu Arg Ala Pro Thr Phe Asp Gln Glu Phe Phe Pro His Gly Val Asn
180 185 190

Val Glu Ile Val Thr Glu Leu Glu Asp Asp Ala Val Ser Met Arg Val
195 200 205

Trp Glu Arg Gly Val Gly Glu Thr Arg Ser Cys Gly Thr Gly Thr Val
210 215 220

Ala Ala Ala Cys Ala Ala Leu Ala Asp Ala Gly Leu Gly Glu Gly Thr
225 230 235 240

Ala Lys Val Cys Val Pro Arg Gly Glu Val Glu Val Gln Ile Phe Asp
245 250 255

Asp Gly Ser Thr Leu Thr Gly Pro Ser Ala Ile Ile Ala Leu Gly Glu
260 265 270

Val Gln Ile
275

<210> 9
<211> 1491
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1468)
<223> RXS02970

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ttatttaaag acttcataat attttgggga gtgaactggt ttg gca ttg aag ggt 115
Leu Ala Leu Lys Gly
1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
10 15 20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
25 30 35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259

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His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
         40                  45                  50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac   307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
     55                  60                  65

atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga   355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
 70                  75                  80                  85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac   403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
                 90                  95                 100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg   451
Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
            105                 110                 115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc   499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
        120                 125                 130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga   547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
    135                 140                 145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga   595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
150                 155                 160                 165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc   643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
                170                 175                 180

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc   691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser
            185                 190                 195

tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag   739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys
        200                 205                 210

cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg   787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala
    215                 220                 225

atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca   835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro
230                 235                 240                 245

gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc   883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile
                250                 255                 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa   931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys
            265                 270                 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc   979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile
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        280                 285                 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc   1027
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
    295                 300                 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc   1075
Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser
310                 315                 320                 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag   1123
Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys
                330                 335                 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct   1171
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala
            345                 350                 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa   1219
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
        360                 365                 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca   1267
Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
    375                 380                 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa   1315
Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
390                 395                 400                 405

ttc aag gaa cgc ggc gtg tgg ccg atg atc tcc ggc aac cga ttc cac   1363
Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser Gly Asn Arg Phe His
                410                 415                 420

atc gcg ccg ccg ctg acc acc act gat gac gaa ttg gta gca ctg ctg   1411
Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu Leu Val Ala Leu Leu
            425                 430                 435

gac gcg gtg gaa gct gca gcc caa gct gtc gag ctg acc ttc gct ggg   1459
Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu Leu Thr Phe Ala Gly
        440                 445                 450

gcg ttg ttc taagttttct agataacaag gcc                            1491
Ala Leu Phe
    455
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<210> 10
<211> 456
<212> PRT
<213> Corynebacterium glutamicum

<400> 10

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Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
             20                  25                  30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
         35                  40                  45
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Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
145 150 155 160

His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
165 170 175

Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
180 185 190

Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
195 200 205

Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
210 215 220

Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
225 230 235 240

Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
245 250 255

Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
260 265 270

Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
275 280 285

Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
290 295 300

Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
305 310 315 320

Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
325 330 335

Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
340 345 350

Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
355 360 365

Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
370 375 380

Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
385 390 395 400

Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly Val Trp Pro Met Ile Ser
405 410 415

Gly Asn Arg Phe His Ile Ala Pro Pro Leu Thr Thr Thr Asp Asp Glu
420 425 430

Leu Val Ala Leu Leu Asp Ala Val Glu Ala Ala Ala Gln Ala Val Glu
435 440 445

Leu Thr Phe Ala Gly Ala Leu Phe
450 455

<210> 11
<211> 1330
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1330)
<223> FRXA01009

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ttatttaaag acttcataat attttgggga gtgaactggt ttg gca ttg aag ggt 115
Leu Ala Leu Lys Gly
1 5

tac acc aac ttt gac ggt gaa ttc atc gaa ttc gga tct gtg caa gca 163
Tyr Thr Asn Phe Asp Gly Glu Phe Ile Glu Phe Gly Ser Val Gln Ala
10 15 20

aaa gaa gag gaa aaa cgg gca ttc gac aac gat cgc gcg cac gtt ttc 211
Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp Arg Ala His Val Phe
25 30 35

cac tcc tgg tcc gcg cag gac aaa atc agc ccc aaa gta tgg gca gct 259
His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro Lys Val Trp Ala Ala
40 45 50

gcc gaa ggt tcc acg ctg tac gac ttc gac ggc aac gcc ttc atc gac 307
Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly Asn Ala Phe Ile Asp
55 60 65

atg ggt tcc caa ctt gtc tcg gca aac tta ggc cac aac aac cct cga 355
Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly His Asn Asn Pro Arg
70 75 80 85

tta gtt gag gcg atc cag cgc caa gca gcc cgg ttg acc aac atc aac 403
Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg Leu Thr Asn Ile Asn
90 95 100

ccg gcc ttc ggc aat gat gtg cgc tct gat gtt gct gca aag atc gtg 451

Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val Ala Ala Lys Ile Val
105 110 115

tcg atg gcc cgt ggc gaa ttc tcc cac gtg ttt ttc acc aac ggc ggc 499
Ser Met Ala Arg Gly Glu Phe Ser His Val Phe Phe Thr Asn Gly Gly
120 125 130

gcc gac gcc atc gag cac tcc atc cgc atg gct cgc ctg cac acc gga 547
Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala Arg Leu His Thr Gly
135 140 145

cgc aac aaa att ctg tcc gca tac cgc agc tac cac ggc gca acc gga 595
Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr His Gly Ala Thr Gly
150 155 160 165

tcc gcg atg atg ctc acc ggc gaa cac cgc cgc ctg ggc aac ccc acc 643
Ser Ala Met Met Leu Thr Gly Glu His Arg Arg Leu Gly Asn Pro Thr
170 175 180

acc gac cca gat atc tac cac ttc tgg gca cca ttc ctg cac cac tcc 691
Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro Phe Leu His His Ser
185 190 195

tca ttc ttt gcc acc acc caa gaa gaa gaa tgc gaa cgc gca ctc aag 739
Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys Glu Arg Ala Leu Lys
200 205 210

cac ttg gaa gat gtc atc gcg ttt gaa ggt gct ggc atg atc gca gcg 787
His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala Gly Met Ile Ala Ala
215 220 225

atc gtc ctg gag cca gtg gtg gga tca tca gga atc atc ctg cca cca 835
Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly Ile Ile Leu Pro Pro
230 235 240 245

gca ggt tac tta aat ggc gtg cgc gaa ctt tgc aac aag cac ggc atc 883
Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys Asn Lys His Gly Ile
250 255 260

ctc ttc atc gcc gac gaa gtc atg gtc gga ttc gga cgc acc gga aaa 931
Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe Gly Arg Thr Gly Lys
265 270 275

ctg ttt gct tac gag cat gct ggc gac gat ttc cag cca gac atg atc 979
Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe Gln Pro Asp Met Ile
280 285 290

acc ttc gcc aag ggt gtt aac gca ggt tac gcc cca ctc ggt ggc atc 1027
Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala Pro Leu Gly Gly Ile
295 300 305

gtg atg acc caa tca atc cgc gat acc ttc gga tca gag gca tac tcc 1075
Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly Ser Glu Ala Tyr Ser
310 315 320 325

ggc gga ctc acc tac tcc gga cac cca ctt gca gta gca ccc gcc aag 1123
Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala Val Ala Pro Ala Lys
330 335 340

gca gcg ctg gag att tac gcg gaa gga gag atc att cca cgc gta gct 1171
Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile Ile Pro Arg Val Ala

345 350 355

cga ctt ggc gct gaa ctg atc gaa cct cgc ctt cgt gaa cta gcg gaa 1219
Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu Arg Glu Leu Ala Glu
360 365 370

gaa aac gta gcg atc gct gac gtg cgg ggc atc gga ttc ttc tgg gca 1267
Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile Gly Phe Phe Trp Ala
375 380 385

gtg gag ttc aat gca gac gcc act gcc atg gct gcc ggt gct gca gaa 1315
Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala Ala Gly Ala Ala Glu
390 395 400 405

ttc aag gaa cgc ggc 1330
Phe Lys Glu Arg Gly
410

<210> 12
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<212> PRT
<213> Corynebacterium glutamicum

<400> 12
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Gly Ser Val Gln Ala Lys Glu Glu Glu Lys Arg Ala Phe Asp Asn Asp
20 25 30

Arg Ala His Val Phe His Ser Trp Ser Ala Gln Asp Lys Ile Ser Pro
35 40 45

Lys Val Trp Ala Ala Ala Glu Gly Ser Thr Leu Tyr Asp Phe Asp Gly
50 55 60

Asn Ala Phe Ile Asp Met Gly Ser Gln Leu Val Ser Ala Asn Leu Gly
65 70 75 80

His Asn Asn Pro Arg Leu Val Glu Ala Ile Gln Arg Gln Ala Ala Arg
85 90 95

Leu Thr Asn Ile Asn Pro Ala Phe Gly Asn Asp Val Arg Ser Asp Val
100 105 110

Ala Ala Lys Ile Val Ser Met Ala Arg Gly Glu Phe Ser His Val Phe
115 120 125

Phe Thr Asn Gly Gly Ala Asp Ala Ile Glu His Ser Ile Arg Met Ala
130 135 140

Arg Leu His Thr Gly Arg Asn Lys Ile Leu Ser Ala Tyr Arg Ser Tyr
145 150 155 160

His Gly Ala Thr Gly Ser Ala Met Met Leu Thr Gly Glu His Arg Arg
165 170 175

Leu Gly Asn Pro Thr Thr Asp Pro Asp Ile Tyr His Phe Trp Ala Pro
180 185 190

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Phe Leu His His Ser Ser Phe Phe Ala Thr Thr Gln Glu Glu Glu Cys
        195                 200                 205

Glu Arg Ala Leu Lys His Leu Glu Asp Val Ile Ala Phe Glu Gly Ala
    210                 215                 220

Gly Met Ile Ala Ala Ile Val Leu Glu Pro Val Val Gly Ser Ser Gly
225                 230                 235                 240

Ile Ile Leu Pro Pro Ala Gly Tyr Leu Asn Gly Val Arg Glu Leu Cys
                245                 250                 255

Asn Lys His Gly Ile Leu Phe Ile Ala Asp Glu Val Met Val Gly Phe
            260                 265                 270

Gly Arg Thr Gly Lys Leu Phe Ala Tyr Glu His Ala Gly Asp Asp Phe
        275                 280                 285

Gln Pro Asp Met Ile Thr Phe Ala Lys Gly Val Asn Ala Gly Tyr Ala
    290                 295                 300

Pro Leu Gly Gly Ile Val Met Thr Gln Ser Ile Arg Asp Thr Phe Gly
305                 310                 315                 320

Ser Glu Ala Tyr Ser Gly Gly Leu Thr Tyr Ser Gly His Pro Leu Ala
                325                 330                 335

Val Ala Pro Ala Lys Ala Ala Leu Glu Ile Tyr Ala Glu Gly Glu Ile
            340                 345                 350

Ile Pro Arg Val Ala Arg Leu Gly Ala Glu Leu Ile Glu Pro Arg Leu
        355                 360                 365

Arg Glu Leu Ala Glu Glu Asn Val Ala Ile Ala Asp Val Arg Gly Ile
    370                 375                 380

Gly Phe Phe Trp Ala Val Glu Phe Asn Ala Asp Ala Thr Ala Met Ala
385                 390                 395                 400

Ala Gly Ala Ala Glu Phe Lys Glu Arg Gly
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<210> 13
<211> 792
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(769)
<223> RXC02390

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ggccgcgagg atctcgtagc tcgcttcgag tcataggccg gtg gag tgg acc gct 115
                                                Val Glu Trp Thr Ala
                                                  1   5

ttt ggc acc ctg att ctg ctc aat ttg gtg ggc agt tta tcc ccg ggg 163

Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly Ser Leu Ser Pro Gly
10 15 20

cct gat acc ttt ttc ctc ctc cgc tta gcc acc cgc tcc aga gcg cac 211
Pro Asp Thr Phe Phe Leu Leu Arg Leu Ala Thr Arg Ser Arg Ala His
25 30 35

gcg atc gct ggc gtc gcc ggc atc gtc acc gga ctc acg gtg tgg gtg 259
Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly Leu Thr Val Trp Val
40 45 50

acg ctg acg gtc gtg gga gca gcg gcg ctg ctc acc act tat ccg tcg 307
Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu Thr Thr Tyr Pro Ser
55 60 65

att ctc gga atc atc cag ctc gtc ggc ggc acg tac cta agc ttc att 355
Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr Tyr Leu Ser Phe Ile
70 75 80 85

ggg tac aag ttg ctg cgc tcg gcg tcg aga gag ctt atc gac gcc cgc 403
Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu Leu Ile Asp Ala Arg
90 95 100

cag ttc cgt ttc aac gcc gat gcc cga cct atc ccg gat gcg gta gaa 451
Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile Pro Asp Ala Val Glu
105 110 115

gca ctg gga acc cgc act cag gta tat cga caa ggt ttg gcc acc aac 499
Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln Gly Leu Ala Thr Asn
120 125 130

ctg tca aac cct aaa gtt gtc atg tac ttc gcg gca att ctg gct ccg 547
Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala Ala Ile Leu Ala Pro
135 140 145

ttg atg cca gcg cac cca tca ccg gtg ctg gcg ttc tct atc atc gtg 595
Leu Met Pro Ala His Pro Ser Pro Val Leu Ala Phe Ser Ile Ile Val
150 155 160 165

gcg att tta gtg cag acc ttt gtt acc ttc tct gct gtg tgc ctc att 643
Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser Ala Val Cys Leu Ile
170 175 180

gtc tct acg gag cgt gtg cgc aaa gca atg ctg cgt gca ggt ccc tgg 691
Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu Arg Ala Gly Pro Trp
185 190 195

ttt gac ctg ctt gct ggc gtt gtc ttc ctc gtt gtg ggt gtg act ctg 739
Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val Val Gly Val Thr Leu
200 205 210

ctg tat gaa ggc ctg acc ggt tta ctc ggg taaaggcata aaaaatggct 789
Leu Tyr Glu Gly Leu Thr Gly Leu Leu Gly
215 220

tcc 792

<210> 14
<211> 223
<212> PRT

<213> Corynebacterium glutamicum

<400> 14

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Val Glu Trp Thr Ala Phe Gly Thr Leu Ile Leu Leu Asn Leu Val Gly
  1               5                  10                  15

Ser Leu Ser Pro Gly Pro Asp Thr Phe Phe Leu Leu Arg Leu Ala Thr
             20                  25                  30

Arg Ser Arg Ala His Ala Ile Ala Gly Val Ala Gly Ile Val Thr Gly
         35                  40                  45

Leu Thr Val Trp Val Thr Leu Thr Val Val Gly Ala Ala Ala Leu Leu
     50                  55                  60

Thr Thr Tyr Pro Ser Ile Leu Gly Ile Ile Gln Leu Val Gly Gly Thr
 65                  70                  75                  80

Tyr Leu Ser Phe Ile Gly Tyr Lys Leu Leu Arg Ser Ala Ser Arg Glu
                 85                  90                  95

Leu Ile Asp Ala Arg Gln Phe Arg Phe Asn Ala Asp Ala Arg Pro Ile
            100                 105                 110

Pro Asp Ala Val Glu Ala Leu Gly Thr Arg Thr Gln Val Tyr Arg Gln
        115                 120                 125

Gly Leu Ala Thr Asn Leu Ser Asn Pro Lys Val Val Met Tyr Phe Ala
    130                 135                 140

Ala Ile Leu Ala Pro Leu Met Pro Ala His Pro Ser Pro Val Leu Ala
145                 150                 155                 160

Phe Ser Ile Ile Val Ala Ile Leu Val Gln Thr Phe Val Thr Phe Ser
                165                 170                 175

Ala Val Cys Leu Ile Val Ser Thr Glu Arg Val Arg Lys Ala Met Leu
            180                 185                 190

Arg Ala Gly Pro Trp Phe Asp Leu Leu Ala Gly Val Val Phe Leu Val
        195                 200                 205

Val Gly Val Thr Leu Leu Tyr Glu Gly Leu Thr Gly Leu Leu Gly
    210                 215                 220
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<210> 15
<211> 897
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(874)
<223> RXC01796

<400> 15

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atgtaactcg atcaggtgga aatgcccgca aaagtggcgg cggtggccga gggatggccg 60

ttggtgcggc atcggtggcc tgctactagt cgggctcttc ttg ctc ctt ggc ggt   115
                                               Leu Leu Leu Gly Gly
```

```
                                            1               5

aac cct gcc gag atc gac cag gtt tta ggt ggc gat caa acc cag atc    163
Asn Pro Ala Glu Ile Asp Gln Val Leu Gly Gly Asp Gln Thr Gln Ile
                10                  15                  20

gag tct gga gag tcc acc gga gcc ggc gac ttt gat cac tgc caa acc    211
Glu Ser Gly Glu Ser Thr Gly Ala Gly Asp Phe Asp His Cys Gln Thr
            25                  30                  35

ggc gca gat gcc aac gcc agt gat gat tgt cgc ctt tac tac acc tca    259
Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg Leu Tyr Tyr Thr Ser
        40                  45                  50

ttc tcc gtc aat gaa atg tgg cag act ttg ctt cca gct cag gct ggt    307
Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu Pro Ala Gln Ala Gly
    55                  60                  65

atc gaa tac acc gag ccg aca ttg act ctt ttc aaa aac tcc acc caa    355
Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe Lys Asn Ser Thr Gln
 70                  75                  80                  85

acc ggc tgc ggt ttc gct tct gcg tcc act ggg ccg ttt tac tgt ccg    403
Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly Pro Phe Tyr Cys Pro
                90                  95                 100

tca gac caa gat gct tat ttt gac ttg act ttc ttc gat cag atg cgt    451
Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe Phe Asp Gln Met Arg
            105                 110                 115

cag ttc ggt gca gaa aac gcc ccg ctt gcc cag atg tac atc gtg gcg    499
Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln Met Tyr Ile Val Ala
        120                 125                 130

cac gag tac ggc cac cac gtc caa aac ctc gag ggc aca ctc gga ctg    547
His Glu Tyr Gly His His Val Gln Asn Leu Glu Gly Thr Leu Gly Leu
    135                 140                 145

tcc aat tac aac gat ccg ggc gct gat tcc aac gcc gtc aag atc gag    595
Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn Ala Val Lys Ile Glu
150                 155                 160                 165

ttg cag gcc gat tgc tac gca ggc att tgg gct aat cac tcc agc gaa    643
Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala Asn His Ser Ser Glu
                170                 175                 180

ggc ccg gat ccg cta ctc caa ccc atc acc gaa tct gag cta gat tcc    691
Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu Ser Glu Leu Asp Ser
            185                 190                 195

gct ctc ctt gct gca agc gcc gtg ggc gac gac aat atc cag caa cga    739
Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp Asn Ile Gln Gln Arg
        200                 205                 210

tcc ggt ggc gat gtc aat cct gaa agc tgg act cac ggc tca tcg cag    787
Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr His Gly Ser Ser Gln
    215                 220                 225

cag cgc aaa gac gcg ttc ctc gcc ggc tac aac acc ggc cag atg agc    835
Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn Thr Gly Gln Met Ser
230                 235                 240                 245
```

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gcc tgc gac ttc ctc ggc cgg ggc gtc tac aac gac gct taaagcattg     884
Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn Asp Ala
                250                 255

cttttcgacg tct                                                     897


<210> 16
<211> 258
<212> PRT
<213> Corynebacterium glutamicum

<400> 16
Leu Leu Leu Gly Gly Asn Pro Ala Glu Ile Asp Gln Val Leu Gly Gly
  1               5                  10                  15

Asp Gln Thr Gln Ile Glu Ser Gly Glu Ser Thr Gly Ala Gly Asp Phe
             20                  25                  30

Asp His Cys Gln Thr Gly Ala Asp Ala Asn Ala Ser Asp Asp Cys Arg
         35                  40                  45

Leu Tyr Tyr Thr Ser Phe Ser Val Asn Glu Met Trp Gln Thr Leu Leu
     50                  55                  60

Pro Ala Gln Ala Gly Ile Glu Tyr Thr Glu Pro Thr Leu Thr Leu Phe
 65                  70                  75                  80

Lys Asn Ser Thr Gln Thr Gly Cys Gly Phe Ala Ser Ala Ser Thr Gly
                 85                  90                  95

Pro Phe Tyr Cys Pro Ser Asp Gln Asp Ala Tyr Phe Asp Leu Thr Phe
            100                 105                 110

Phe Asp Gln Met Arg Gln Phe Gly Ala Glu Asn Ala Pro Leu Ala Gln
        115                 120                 125

Met Tyr Ile Val Ala His Glu Tyr Gly His His Val Gln Asn Leu Glu
    130                 135                 140

Gly Thr Leu Gly Leu Ser Asn Tyr Asn Asp Pro Gly Ala Asp Ser Asn
145                 150                 155                 160

Ala Val Lys Ile Glu Leu Gln Ala Asp Cys Tyr Ala Gly Ile Trp Ala
                165                 170                 175

Asn His Ser Ser Glu Gly Pro Asp Pro Leu Leu Gln Pro Ile Thr Glu
            180                 185                 190

Ser Glu Leu Asp Ser Ala Leu Leu Ala Ala Ser Ala Val Gly Asp Asp
        195                 200                 205

Asn Ile Gln Gln Arg Ser Gly Gly Asp Val Asn Pro Glu Ser Trp Thr
    210                 215                 220

His Gly Ser Ser Gln Gln Arg Lys Asp Ala Phe Leu Ala Gly Tyr Asn
225                 230                 235                 240

Thr Gly Gln Met Ser Ala Cys Asp Phe Leu Gly Arg Gly Val Tyr Asn
                245                 250                 255
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Asp Ala

<210> 17
<211> 771
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(748)
<223> RXC01207

<400> 17
cttcatgatc tcaccggcag agcgcgtttt gttacagcgc gtaaactgtg actttgaaaa 60

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atttttgaac aatccgtaca ccaacttcag gagaaaaaca gtg agc aga atc tat   115
                                              Val Ser Arg Ile Tyr
                                                1               5

gac tgt gcc gac caa gac tcc cgt gca gca ggc cta aag gcg gct gtc   163
Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly Leu Lys Ala Ala Val
                10                  15                  20

gat gca gtc aaa gcc ggt cag ctc gtt gtc ctt ccc acg gat acc ctt   211
Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu Pro Thr Asp Thr Leu
            25                  30                  35

tat gga ctc ggc tgc gac gct ttc aac aac gag gca gta gcc aac ctt   259
Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu Ala Val Ala Asn Leu
        40                  45                  50

ctg gcc acc aaa cac cgt ggc ccc gat atg ccc gtt cca gtg ctc gtc   307
Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro Val Pro Val Leu Val
    55                  60                  65

ggc agc tgg gac acc att caa gga ctt gtg cac tcc tat tct gcg cag   355
Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His Ser Tyr Ser Ala Gln
70                  75                  80                  85

gca aaa gcg ctt gtg gag gcg ttc tgg cct ggt gga ctg tcc atc atc   403
Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly Gly Leu Ser Ile Ile
                90                  95                 100

gtt ccg cag gca cca agc ctt ccg tgg aac ctt ggc gat acc cgt ggc   451
Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu Gly Asp Thr Arg Gly
            105                 110                 115

acc gta atg ctg cgc atg cca ctg cac cca gtt gcc att gaa ttg ctg   499
Thr Val Met Leu Arg Met Pro Leu His Pro Val Ala Ile Glu Leu Leu
        120                 125                 130

cgc caa acc gga cca atg gct gtc tcc tcc gcc aac atc tcc gga cat   547
Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala Asn Ile Ser Gly His
    135                 140                 145

act cct cca acc acc gtg ctg gag gct cgt cag cag ctc aac caa aat   595
Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln Gln Leu Asn Gln Asn
150                 155                 160                 165
```

```
gtc gct gtc tac ctc gat ggt ggc gaa tgc gcg ctg gcc acc cct tca      643
Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala Leu Ala Thr Pro Ser
                170                 175                 180

acc atc gtg gat att tca ggc ccc gca cca aag att ttg cgt gag ggt      691
Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys Ile Leu Arg Glu Gly
            185                 190                 195

gcc atc agc gca gaa cgc gtt ggc gaa gta ctt gga gtg tcg gca gaa      739
Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu Gly Val Ser Ala Glu
        200                 205                 210

agc ctg cgc taaatgggag tcggtttcgc ggg                                771
Ser Leu Arg
    215


<210> 18
<211> 216
<212> PRT
<213> Corynebacterium glutamicum

<400> 18
Val Ser Arg Ile Tyr Asp Cys Ala Asp Gln Asp Ser Arg Ala Ala Gly
 1               5                  10                  15

Leu Lys Ala Ala Val Asp Ala Val Lys Ala Gly Gln Leu Val Val Leu
            20                  25                  30

Pro Thr Asp Thr Leu Tyr Gly Leu Gly Cys Asp Ala Phe Asn Asn Glu
        35                  40                  45

Ala Val Ala Asn Leu Leu Ala Thr Lys His Arg Gly Pro Asp Met Pro
    50                  55                  60

Val Pro Val Leu Val Gly Ser Trp Asp Thr Ile Gln Gly Leu Val His
65                  70                  75                  80

Ser Tyr Ser Ala Gln Ala Lys Ala Leu Val Glu Ala Phe Trp Pro Gly
                85                  90                  95

Gly Leu Ser Ile Ile Val Pro Gln Ala Pro Ser Leu Pro Trp Asn Leu
            100                 105                 110

Gly Asp Thr Arg Gly Thr Val Met Leu Arg Met Pro Leu His Pro Val
        115                 120                 125

Ala Ile Glu Leu Leu Arg Gln Thr Gly Pro Met Ala Val Ser Ser Ala
    130                 135                 140

Asn Ile Ser Gly His Thr Pro Pro Thr Thr Val Leu Glu Ala Arg Gln
145                 150                 155                 160

Gln Leu Asn Gln Asn Val Ala Val Tyr Leu Asp Gly Gly Glu Cys Ala
                165                 170                 175

Leu Ala Thr Pro Ser Thr Ile Val Asp Ile Ser Gly Pro Ala Pro Lys
            180                 185                 190

Ile Leu Arg Glu Gly Ala Ile Ser Ala Glu Arg Val Gly Glu Val Leu
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```
        195                 200                 205

Gly Val Ser Ala Glu Ser Leu Arg
    210                 215


<210> 19
<211> 1026
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1003)
<223> RXC00657

<400> 19
gtgcggatcg ggtatccgcg ctacacttag aggtgttaga gatcatgagt ttccacgaac 60

tgtaacgcag gattcaccaa tcaatgaaag gtcgaccgac atg agc act gaa gac   115
                                            Met Ser Thr Glu Asp
                                              1               5

att gtc gtc gta gca gta gat ggc tcg gac gcc tca aaa caa gct gtt   163
Ile Val Val Val Ala Val Asp Gly Ser Asp Ala Ser Lys Gln Ala Val
                 10                  15                  20

cgg tgg gct gca aat acc gcc aac aaa cgt ggc att cca ctt cgc ttg   211
Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly Ile Pro Leu Arg Leu
             25                  30                  35

gct tcc agc tac acc atg cct cag ttc ctc tac gca gag gga atg gtt   259
Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr Ala Glu Gly Met Val
         40                  45                  50

cca cca caa gag ctt ttc gat gac ctc cag gcc gaa gcc ctg gaa aag   307
Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala Glu Ala Leu Glu Lys
     55                  60                  65

att aac gaa gcc cgt gac atc gcc cat gag gta gcg cca gaa atc aag   355
Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val Ala Pro Glu Ile Lys
 70                  75                  80                  85

atc ggg cac acc atc gct gaa ggc agt ccc atc gac atg ctg ttg gaa   403
Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile Asp Met Leu Leu Glu
                 90                  95                 100

atg tct ccc gat gcc aca atg atc gtc atg ggt tcc cgc gga ctc ggc   451
Met Ser Pro Asp Ala Thr Met Ile Val Met Gly Ser Arg Gly Leu Gly
             105                 110                 115

gga ctc tcc gga atg gtc atg ggc tcc gtc tcc ggt gca gtg gtc agc   499
Gly Leu Ser Gly Met Val Met Gly Ser Val Ser Gly Ala Val Val Ser
         120                 125                 130

cac gca aag tgt cca gtc gtt gtt gtc cgt gaa gac agc gca gtc aac   547
His Ala Lys Cys Pro Val Val Val Val Arg Glu Asp Ser Ala Val Asn
    135                 140                 145

gaa gac agc aag tac ggc cca gtc gtc gtc ggt gtg gat ggc tcc gaa   595
Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly Val Asp Gly Ser Glu
```

150 155 160 165

gtc tcc caa cag gca acc gaa tac gca ttt gcg gaa gct gaa gct cgt 643
Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala Glu Ala Glu Ala Arg
170 175 180

ggc gcc gaa ctc gtt gca gtt cac acc tgg atg gac atg cag gta cag 691
Gly Ala Glu Leu Val Ala Val His Thr Trp Met Asp Met Gln Val Gln
185 190 195

gca tca ctt gca ggt ctt gca gct gct caa cag cag tgg gat gaa gtg 739
Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln Gln Trp Asp Glu Val
200 205 210

gaa cgt cag caa acc gac atg ctg atc gaa cgc ctc gca cca ctg gtg 787
Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg Leu Ala Pro Leu Val
215 220 225

gaa aag tac cca agt gta acc gtc aag aag atc atc acc cgt gac cgc 835
Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile Ile Thr Arg Asp Arg
230 235 240 245

cca gtt cgc gca ctt gca gaa gca tct gaa aac gcg cag ctc cta gtc 883
Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn Ala Gln Leu Leu Val
250 255 260

gtt ggt tcc cat ggt cgt ggc gga ttt aag ggc atg ctc ctt ggc tcc 931
Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly Met Leu Leu Gly Ser
265 270 275

acc tcc cgc gca ctg ctg caa tcc gca ccg tgc cca atg atg gtg gtt 979
Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys Pro Met Met Val Val
280 285 290

cgc cca cct gag aag att aag aag tagtttcttt taagtttcga tgc 1026
Arg Pro Pro Glu Lys Ile Lys Lys
295 300

<210> 20
<211> 301
<212> PRT
<213> Corynebacterium glutamicum

<400> 20
Met Ser Thr Glu Asp Ile Val Val Val Ala Val Asp Gly Ser Asp Ala
1 5 10 15

Ser Lys Gln Ala Val Arg Trp Ala Ala Asn Thr Ala Asn Lys Arg Gly
20 25 30

Ile Pro Leu Arg Leu Ala Ser Ser Tyr Thr Met Pro Gln Phe Leu Tyr
35 40 45

Ala Glu Gly Met Val Pro Pro Gln Glu Leu Phe Asp Asp Leu Gln Ala
50 55 60

Glu Ala Leu Glu Lys Ile Asn Glu Ala Arg Asp Ile Ala His Glu Val
65 70 75 80

Ala Pro Glu Ile Lys Ile Gly His Thr Ile Ala Glu Gly Ser Pro Ile

```
                85                  90                  95

Asp Met Leu Leu Glu Met Ser Pro Asp Ala Thr Met Ile Val Met Gly
            100                 105                 110

Ser Arg Gly Leu Gly Gly Leu Ser Gly Met Val Met Gly Ser Val Ser
        115                 120                 125

Gly Ala Val Val Ser His Ala Lys Cys Pro Val Val Val Val Arg Glu
    130                 135                 140

Asp Ser Ala Val Asn Glu Asp Ser Lys Tyr Gly Pro Val Val Val Gly
145                 150                 155                 160

Val Asp Gly Ser Glu Val Ser Gln Gln Ala Thr Glu Tyr Ala Phe Ala
                165                 170                 175

Glu Ala Glu Ala Arg Gly Ala Glu Leu Val Ala Val His Thr Trp Met
            180                 185                 190

Asp Met Gln Val Gln Ala Ser Leu Ala Gly Leu Ala Ala Ala Gln Gln
        195                 200                 205

Gln Trp Asp Glu Val Glu Arg Gln Gln Thr Asp Met Leu Ile Glu Arg
    210                 215                 220

Leu Ala Pro Leu Val Glu Lys Tyr Pro Ser Val Thr Val Lys Lys Ile
225                 230                 235                 240

Ile Thr Arg Asp Arg Pro Val Arg Ala Leu Ala Glu Ala Ser Glu Asn
                245                 250                 255

Ala Gln Leu Leu Val Val Gly Ser His Gly Arg Gly Gly Phe Lys Gly
            260                 265                 270

Met Leu Leu Gly Ser Thr Ser Arg Ala Leu Leu Gln Ser Ala Pro Cys
        275                 280                 285

Pro Met Met Val Val Arg Pro Pro Glu Lys Ile Lys Lys
    290                 295                 300
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<210> 21
<211> 1059
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1036)
<223> RXC00552

<400> 21
ccgccaacaa ggcagcaaag ctcgatccaa ttgacgcctt gcgttatgag taaaagcctc 60

gtttttaagg tagccacaca tcgcactaga ctgaagaact gtg gct acc tca aaa 115
                                                Val Ala Thr Ser Lys
                                                  1   5

att ctt ctt tat tac gca ttc acc ccg ctc tct gac cct aaa gcg gtt 163
Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser Asp Pro Lys Ala Val

```
                 10                       15                       20

cag ctg tgg cag cgt gag ctc tgc gag tca ctg aat ctt cgt ggc cgc    211
Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu Asn Leu Arg Gly Arg
            25                  30                  35

atc ctg atc tcc act cac ggc atc aat gga acc gtg ggc gga gat att    259
Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr Val Gly Gly Asp Ile
        40                  45                  50

gat gat tgc aag gcg tac att aaa aag acc cgc gag tac cca ggt ttc    307
Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg Glu Tyr Pro Gly Phe
    55                  60                  65

aac cgc atg cag ttt aag tgg tcc gag ggt ggc gct gag gat ttc cca    355
Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly Ala Glu Asp Phe Pro
70                  75                  80                  85

aag ctc agt gtc aaa gtc cgc gat gag atc gtt gcc ttc ggc gct cca    403
Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val Ala Phe Gly Ala Pro
                90                  95                  100

gat gag ctc aaa gtg gat gaa aac ggc gtc gtc ggt ggc ggc gtt cac    451
Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val Gly Gly Gly Val His
            105                 110                 115

ctg aaa cca cag cag gtc aat gag ctt gtg gaa gcc cgt ggc gat gaa    499
Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu Ala Arg Gly Asp Glu
        120                 125                 130

gtt gtg ttc ttt gac ggc cgc aac gca atg gaa gcc cag atc ggc aag    547
Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu Ala Gln Ile Gly Lys
    135                 140                 145

ttc aag gac gct gtt gtc cct gac gta gaa acc act cat gat ttc atc    595
Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr Thr His Asp Phe Ile
150                 155                 160                 165

gca gaa att gag tct gga aaa tac gac gat ctc aaa gac aag cct gtg    643
Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu Lys Asp Lys Pro Val
                170                 175                 180

gtc acc tac tgc acc ggc gga att cgt tgt gag atc ctg agt tca ctc    691
Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu Ile Leu Ser Ser Leu
            185                 190                 195

atg atc aac cgt ggt ttc aaa gag gtc tac caa atc gat ggc ggc atc    739
Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln Ile Asp Gly Gly Ile
        200                 205                 210

gtt cgc tac ggc gag cag ttt ggc aac aag ggc ctg tgg gaa ggc tcc    787
Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly Leu Trp Glu Gly Ser
    215                 220                 225

ctc tac gtt ttc gat aag cgc atg cat atg gaa ttc ggc gag gat tac    835
Leu Tyr Val Phe Asp Lys Arg Met His Met Glu Phe Gly Glu Asp Tyr
230                 235                 240                 245

aaa gag gtc gga cac tgc atc cat tgc gat act ccc acc aac aaa ttt    883
Lys Glu Val Gly His Cys Ile His Cys Asp Thr Pro Thr Asn Lys Phe
                250                 255                 260
```

```
gag cac tgc ctc aac gaa gat gat tgc cgc gag ctc gtg ttg atg tgc     931
Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu Leu Val Leu Met Cys
            265                 270                 275

cct gat tgc ttc gcc aat gtt gag acc cgt cat tgc aag cgc gaa cgc     979
Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His Cys Lys Arg Glu Arg
        280                 285                 290

tgt gca gca att gct gcg gat ttc gct gag caa gga att gat ccg ctc     1027
Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln Gly Ile Asp Pro Leu
    295                 300                 305

gtt act tct taaaaagggt atggtggctg ggt                               1059
Val Thr Ser
310


<210> 22
<211> 312
<212> PRT
<213> Corynebacterium glutamicum

<400> 22
Val Ala Thr Ser Lys Ile Leu Leu Tyr Tyr Ala Phe Thr Pro Leu Ser
  1               5                  10                  15

Asp Pro Lys Ala Val Gln Leu Trp Gln Arg Glu Leu Cys Glu Ser Leu
            20                  25                  30

Asn Leu Arg Gly Arg Ile Leu Ile Ser Thr His Gly Ile Asn Gly Thr
        35                  40                  45

Val Gly Gly Asp Ile Asp Asp Cys Lys Ala Tyr Ile Lys Lys Thr Arg
    50                  55                  60

Glu Tyr Pro Gly Phe Asn Arg Met Gln Phe Lys Trp Ser Glu Gly Gly
 65                  70                  75                  80

Ala Glu Asp Phe Pro Lys Leu Ser Val Lys Val Arg Asp Glu Ile Val
                85                  90                  95

Ala Phe Gly Ala Pro Asp Glu Leu Lys Val Asp Glu Asn Gly Val Val
            100                 105                 110

Gly Gly Gly Val His Leu Lys Pro Gln Gln Val Asn Glu Leu Val Glu
        115                 120                 125

Ala Arg Gly Asp Glu Val Val Phe Phe Asp Gly Arg Asn Ala Met Glu
    130                 135                 140

Ala Gln Ile Gly Lys Phe Lys Asp Ala Val Val Pro Asp Val Glu Thr
145                 150                 155                 160

Thr His Asp Phe Ile Ala Glu Ile Glu Ser Gly Lys Tyr Asp Asp Leu
                165                 170                 175

Lys Asp Lys Pro Val Val Thr Tyr Cys Thr Gly Gly Ile Arg Cys Glu
            180                 185                 190

Ile Leu Ser Ser Leu Met Ile Asn Arg Gly Phe Lys Glu Val Tyr Gln
```

```
        195                 200                 205

Ile Asp Gly Gly Ile Val Arg Tyr Gly Glu Gln Phe Gly Asn Lys Gly
    210                 215                 220

Leu Trp Glu Gly Ser Leu Tyr Val Phe Asp Lys Arg Met His Met Glu
225                 230                 235                 240

Phe Gly Glu Asp Tyr Lys Glu Val Gly His Cys Ile His Cys Asp Thr
                245                 250                 255

Pro Thr Asn Lys Phe Glu His Cys Leu Asn Glu Asp Asp Cys Arg Glu
            260                 265                 270

Leu Val Leu Met Cys Pro Asp Cys Phe Ala Asn Val Glu Thr Arg His
        275                 280                 285

Cys Lys Arg Glu Arg Cys Ala Ala Ile Ala Ala Asp Phe Ala Glu Gln
    290                 295                 300

Gly Ile Asp Pro Leu Val Thr Ser
305                 310


<210> 23
<211> 1386
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1363)
<223> RXA00534

<400> 23
ctgtgcagaa agaaaacact cctctggcta ggtagacaca gtttataaag gtagagttga 60

gcgggtaact gtcagcacgt agatcgaaag gtgcacaaag gtg gcc ctg gtc gta   115
                                           Val Ala Leu Val Val
                                           1               5

cag aaa tat ggc ggt tcc tcg ctt gag agt gcg gaa cgc att aga aac   163
Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala Glu Arg Ile Arg Asn
                10                  15                  20

gtc gct gaa cgg atc gtt gcc acc aag aag gct gga aat gat gtc gtg   211
Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala Gly Asn Asp Val Val
            25                  30                  35

gtt gtc tgc tcc gca atg gga gac acc acg gat gaa ctt cta gaa ctt   259
Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp Glu Leu Leu Glu Leu
        40                  45                  50

gca gcg gca gtg aat ccc gtt ccg cca gct cgt gaa atg gat atg ctc   307
Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg Glu Met Asp Met Leu
    55                  60                  65

ctg act gct ggt gag cgt att tct aac gct ctc gtc gcc atg gct att   355
Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu Val Ala Met Ala Ile
70                  75                  80                  85
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```
gag tcc ctt ggc gca gaa gcc caa tct ttc acg ggc tct cag gct ggt    403
Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr Gly Ser Gln Ala Gly
                 90                  95                 100

gtg ctc acc acc gag cgc cac gga aac gca cgc att gtt gat gtc act    451
Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg Ile Val Asp Val Thr
            105                 110                 115

cca ggt cgt gtg cgt gaa gca ctc gat gag ggc aag atc tgc att gtt    499
Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly Lys Ile Cys Ile Val
        120                 125                 130

gct ggt ttc cag ggt gtt aat aaa gaa acc cgc gat gtc acc acg ttg    547
Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg Asp Val Thr Thr Leu
    135                 140                 145

ggt cgt ggt ggt tct gac acc act gca gtt gcg ttg gca gct gct ttg    595
Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala Leu Ala Ala Ala Leu
150                 155                 160                 165

aac gct gat gtg tgt gag att tac tcg gac gtt gac ggt gtg tat acc    643
Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val Asp Gly Val Tyr Thr
                170                 175                 180

gct gac ccg cgc atc gtt cct aat gca cag aag ctg gaa aag ctc agc    691
Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys Leu Glu Lys Leu Ser
            185                 190                 195

ttc gaa gaa atg ctg gaa ctt gct gct gtt ggc tcc aag att ttg gtg    739
Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly Ser Lys Ile Leu Val
        200                 205                 210

ctg cgc agt gtt gaa tac gct cgt gca ttc aat gtg cca ctt cgc gta    787
Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn Val Pro Leu Arg Val
    215                 220                 225

cgc tcg tct tat agt aat gat ccc ggc act ttg att gcc ggc tct atg    835
Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu Ile Ala Gly Ser Met
230                 235                 240                 245

gag gat att cct gtg gaa gaa gca gtc ctt acc ggt gtc gca acc gac    883
Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr Gly Val Ala Thr Asp
                250                 255                 260

aag tcc gaa gcc aaa gta acc gtt ctg ggt att tcc gat aag cca ggc    931
Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile Ser Asp Lys Pro Gly
            265                 270                 275

gag gct gcg aag gtt ttc cgt gcg ttg gct gat gca gaa atc aac att    979
Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp Ala Glu Ile Asn Ile
        280                 285                 290

gac atg gtt ctg cag aac gtc tct tct gta gaa gac ggc acc acc gac    1027
Asp Met Val Leu Gln Asn Val Ser Ser Val Glu Asp Gly Thr Thr Asp
    295                 300                 305

atc acc ttc acc tgc cct cgt tcc gac ggc cgc cgc gcg atg gag atc    1075
Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg Arg Ala Met Glu Ile
310                 315                 320                 325

ttg aag aag ctt cag gtt cag ggc aac tgg acc aat gtg ctt tac gac    1123
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Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr Asn Val Leu Tyr Asp
                330                 335                 340

gac cag gtc ggc aaa gtc tcc ctc gtg ggt gct ggc atg aag tct cac   1171
Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala Gly Met Lys Ser His
            345                 350                 355

cca ggt gtt acc gca gag ttc atg gaa gct ctg cgc gat gtc aac gtg   1219
Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu Arg Asp Val Asn Val
        360                 365                 370

aac atc gaa ttg att tcc acc tct gag att cgt att tcc gtg ctg atc   1267
Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg Ile Ser Val Leu Ile
    375                 380                 385

cgt gaa gat gat ctg gat gct gct gca cgt gca ttg cat gag cag ttc   1315
Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala Leu His Glu Gln Phe
390                 395                 400                 405

cag ctg ggc ggc gaa gac gaa gcc gtc gtt tat gca ggc acc gga cgc   1363
Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr Ala Gly Thr Gly Arg
                410                 415                 420

taaagtttta aaggagtagt ttt                                        1386


<210> 24
<211> 421
<212> PRT
<213> Corynebacterium glutamicum

<400> 24
Val Ala Leu Val Val Gln Lys Tyr Gly Gly Ser Ser Leu Glu Ser Ala
  1               5                  10                  15

Glu Arg Ile Arg Asn Val Ala Glu Arg Ile Val Ala Thr Lys Lys Ala
             20                  25                  30

Gly Asn Asp Val Val Val Val Cys Ser Ala Met Gly Asp Thr Thr Asp
         35                  40                  45

Glu Leu Leu Glu Leu Ala Ala Ala Val Asn Pro Val Pro Pro Ala Arg
     50                  55                  60

Glu Met Asp Met Leu Leu Thr Ala Gly Glu Arg Ile Ser Asn Ala Leu
 65                  70                  75                  80

Val Ala Met Ala Ile Glu Ser Leu Gly Ala Glu Ala Gln Ser Phe Thr
                 85                  90                  95

Gly Ser Gln Ala Gly Val Leu Thr Thr Glu Arg His Gly Asn Ala Arg
            100                 105                 110

Ile Val Asp Val Thr Pro Gly Arg Val Arg Glu Ala Leu Asp Glu Gly
        115                 120                 125

Lys Ile Cys Ile Val Ala Gly Phe Gln Gly Val Asn Lys Glu Thr Arg
    130                 135                 140

Asp Val Thr Thr Leu Gly Arg Gly Gly Ser Asp Thr Thr Ala Val Ala
145                 150                 155                 160
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Leu Ala Ala Ala Leu Asn Ala Asp Val Cys Glu Ile Tyr Ser Asp Val
165 170 175

Asp Gly Val Tyr Thr Ala Asp Pro Arg Ile Val Pro Asn Ala Gln Lys
180 185 190

Leu Glu Lys Leu Ser Phe Glu Glu Met Leu Glu Leu Ala Ala Val Gly
195 200 205

Ser Lys Ile Leu Val Leu Arg Ser Val Glu Tyr Ala Arg Ala Phe Asn
210 215 220

Val Pro Leu Arg Val Arg Ser Ser Tyr Ser Asn Asp Pro Gly Thr Leu
225 230 235 240

Ile Ala Gly Ser Met Glu Asp Ile Pro Val Glu Glu Ala Val Leu Thr
245 250 255

Gly Val Ala Thr Asp Lys Ser Glu Ala Lys Val Thr Val Leu Gly Ile
260 265 270

Ser Asp Lys Pro Gly Glu Ala Ala Lys Val Phe Arg Ala Leu Ala Asp
275 280 285

Ala Glu Ile Asn Ile Asp Met Val Leu Gln Asn Val Ser Ser Val Glu
290 295 300

Asp Gly Thr Thr Asp Ile Thr Phe Thr Cys Pro Arg Ser Asp Gly Arg
305 310 315 320

Arg Ala Met Glu Ile Leu Lys Lys Leu Gln Val Gln Gly Asn Trp Thr
325 330 335

Asn Val Leu Tyr Asp Asp Gln Val Gly Lys Val Ser Leu Val Gly Ala
340 345 350

Gly Met Lys Ser His Pro Gly Val Thr Ala Glu Phe Met Glu Ala Leu
355 360 365

Arg Asp Val Asn Val Asn Ile Glu Leu Ile Ser Thr Ser Glu Ile Arg
370 375 380

Ile Ser Val Leu Ile Arg Glu Asp Asp Leu Asp Ala Ala Ala Arg Ala
385 390 395 400

Leu His Glu Gln Phe Gln Leu Gly Gly Glu Asp Glu Ala Val Val Tyr
405 410 415

Ala Gly Thr Gly Arg
420

<210> 25
<211> 1155
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1132)

<223> RXA00533

<400> 25

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caggcaccgg acgctaaagt tttaaaggag tagttttaca atg acc acc atc gca   115
                                            Met Thr Thr Ile Ala
                                              1               5

gtt gtt ggt gca acc ggc cag gtc ggc cag gtt atg cgc acc ctt ttg   163
Val Val Gly Ala Thr Gly Gln Val Gly Gln Val Met Arg Thr Leu Leu
                 10                  15                  20

gaa gag cgc aat ttc cca gct gac act gtt cgt ttc ttt gct tcc cca   211
Glu Glu Arg Asn Phe Pro Ala Asp Thr Val Arg Phe Phe Ala Ser Pro
             25                  30                  35

cgt tcc gca ggc cgt aag att gaa ttc cgt ggc acg gaa atc gag gta   259
Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly Thr Glu Ile Glu Val
         40                  45                  50

gaa gac att act cag gca acc gag gag tcc ctc aag gac atc gac gtt   307
Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu Lys Asp Ile Asp Val
     55                  60                  65

gcg ttg ttc tcc gct gga ggc acc gct tcc aag cag tac gct cca ctg   355
Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys Gln Tyr Ala Pro Leu
 70                  75                  80                  85

ttc gct gct gca ggc gcg act gtt gtg gat aac tct tct gct tgg cgc   403
Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn Ser Ser Ala Trp Arg
                 90                  95                 100

aag gac gac gag gtt cca cta atc gtc tct gag gtg aac cct tcc gac   451
Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu Val Asn Pro Ser Asp
             105                 110                 115

aag gat tcc ctg gtc aag ggc att att gcg aac cct aac tgc acc acc   499
Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn Pro Asn Cys Thr Thr
         120                 125                 130

atg gct gcg atg cca gtg ctg aag cca ctt cac gat gcc gct ggt ctt   547
Met Ala Ala Met Pro Val Leu Lys Pro Leu His Asp Ala Ala Gly Leu
     135                 140                 145

gta aag ctt cac gtt tcc tct tac cag gct gtt tcc ggt tct ggt ctt   595
Val Lys Leu His Val Ser Ser Tyr Gln Ala Val Ser Gly Ser Gly Leu
150                 155                 160                 165

gca ggt gtg gaa acc ttg gca aag cag gtt gct gca gtt gga gac cac   643
Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala Ala Val Gly Asp His
                 170                 175                 180

aac gtt gag ttc gtc cat gat gga cag gct gct gac gca ggc gat gtc   691
Asn Val Glu Phe Val His Asp Gly Gln Ala Ala Asp Ala Gly Asp Val
             185                 190                 195

gga cct tat gtt tca cca atc gct tac aac gtg ctg cca ttc gcc gga   739
Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val Leu Pro Phe Ala Gly
         200                 205                 210
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aac ctc gtc gat gac ggc acc ttc gaa acc gat gaa gag cag aag ctg 787
Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp Glu Glu Gln Lys Leu
215 220 225

cgc aac gaa tcc cgc aag att ctc ggt ctc cca gac ctc aag gtc tca 835
Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro Asp Leu Lys Val Ser
230 235 240 245

ggc acc tgc gtc cgc gtg ccg gtt ttc acc ggc cac acg ctg acc att 883
Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly His Thr Leu Thr Ile
250 255 260

cac gcc gaa ttc gac aag gca atc acc gtg gac cag gcg cag gag atc 931
His Ala Glu Phe Asp Lys Ala Ile Thr Val Asp Gln Ala Gln Glu Ile
265 270 275

ttg ggt gcc gct tca ggc gtc aag ctt gtc gac gtc cca acc cca ctt 979
Leu Gly Ala Ala Ser Gly Val Lys Leu Val Asp Val Pro Thr Pro Leu
280 285 290

gca gct gcc ggc att gac gaa tcc ctc gtt gga cgc atc cgt cag gac 1027
Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly Arg Ile Arg Gln Asp
295 300 305

tcc act gtc gac gat aac cgc ggt ctg gtt ctc gtc gta tct ggc gac 1075
Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu Val Val Ser Gly Asp
310 315 320 325

aac ctc cgc aag ggt gct gcg cta aac acc atc cag atc gct gag ctg 1123
Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile Gln Ile Ala Glu Leu
330 335 340

ctg gtt aag taaaaacccg ccattaaaaa ctc 1155
Leu Val Lys

<210> 26
<211> 344
<212> PRT
<213> Corynebacterium glutamicum

<400> 26
Met Thr Thr Ile Ala Val Val Gly Ala Thr Gly Gln Val Gly Gln Val
1 5 10 15

Met Arg Thr Leu Leu Glu Glu Arg Asn Phe Pro Ala Asp Thr Val Arg
20 25 30

Phe Phe Ala Ser Pro Arg Ser Ala Gly Arg Lys Ile Glu Phe Arg Gly
35 40 45

Thr Glu Ile Glu Val Glu Asp Ile Thr Gln Ala Thr Glu Glu Ser Leu
50 55 60

Lys Asp Ile Asp Val Ala Leu Phe Ser Ala Gly Gly Thr Ala Ser Lys
65 70 75 80

Gln Tyr Ala Pro Leu Phe Ala Ala Ala Gly Ala Thr Val Val Asp Asn
85 90 95

Ser Ser Ala Trp Arg Lys Asp Asp Glu Val Pro Leu Ile Val Ser Glu
100 105 110

Val Asn Pro Ser Asp Lys Asp Ser Leu Val Lys Gly Ile Ile Ala Asn
115 120 125

Pro Asn Cys Thr Thr Met Ala Ala Met Pro Val Leu Lys Pro Leu His
130 135 140

Asp Ala Ala Gly Leu Val Lys Leu His Val Ser Ser Tyr Gln Ala Val
145 150 155 160

Ser Gly Ser Gly Leu Ala Gly Val Glu Thr Leu Ala Lys Gln Val Ala
165 170 175

Ala Val Gly Asp His Asn Val Glu Phe Val His Asp Gly Gln Ala Ala
180 185 190

Asp Ala Gly Asp Val Gly Pro Tyr Val Ser Pro Ile Ala Tyr Asn Val
195 200 205

Leu Pro Phe Ala Gly Asn Leu Val Asp Asp Gly Thr Phe Glu Thr Asp
210 215 220

Glu Glu Gln Lys Leu Arg Asn Glu Ser Arg Lys Ile Leu Gly Leu Pro
225 230 235 240

Asp Leu Lys Val Ser Gly Thr Cys Val Arg Val Pro Val Phe Thr Gly
245 250 255

His Thr Leu Thr Ile His Ala Glu Phe Asp Lys Ala Ile Thr Val Asp
260 265 270

Gln Ala Gln Glu Ile Leu Gly Ala Ala Ser Gly Val Lys Leu Val Asp
275 280 285

Val Pro Thr Pro Leu Ala Ala Ala Gly Ile Asp Glu Ser Leu Val Gly
290 295 300

Arg Ile Arg Gln Asp Ser Thr Val Asp Asp Asn Arg Gly Leu Val Leu
305 310 315 320

Val Val Ser Gly Asp Asn Leu Arg Lys Gly Ala Ala Leu Asn Thr Ile
325 330 335

Gln Ile Ala Glu Leu Leu Val Lys
340

<210> 27
<211> 608
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (69)..(608)
<223> RXA02843

<400> 27
cccattgcgc ggaggtcgca ccccttccga cttgaactga taggccgata gaaattattc 60

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tggacgtc atg act act gct tcc gca acc gga att gca aca ctg acc tcc  110
         Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser
          1               5                  10

acc ggc gac gtc ctg gac gtg tgg tat cca gaa atc ggg tcc acc gac  158
Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp
 15                  20                  25                  30

cag tcc gcg ctc aca cct cta gaa ggc gtc gat gaa gat cga aac gtc  206
Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val
                 35                  40                  45

acc cgc aaa atc gtg acg aca act atc gac acc gac gca gcc ccc acc  254
Thr Arg Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr
             50                  55                  60

gac acc tac gat gca tgg ctg cgc ctt cac ctc ctc tcc cac cgc gtt  302
Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val
         65                  70                  75

ttc cgc cct cac acc atc aac cta gac ggc att ttc ggc ctc ctc aac  350
Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn
     80                  85                  90

aat gtc gtg tgg acc aac ttc gga ccg tgc gca gtt gac ggt ttc gca  398
Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala
 95                  100                 105                 110

ctc acc cgc gcg cgc ctg tca cgc cga ggc caa gtt acg gtt tat agc  446
Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser
                115                 120                 125

gtc gac aag ttc cca cgc atg gtc gac tat gtg gtt ccc tcg ggc gtg  494
Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val
            130                 135                 140

cgc atc ggt gac gcc gac cgc gtc cga ctt ggc gcg tac ctg gca gat  542
Arg Ile Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp
        145                 150                 155

ggc acc acc gtg atg cat gag ggc ttc gtg aac ttc aac gct ggc acg  590
Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr
    160                 165                 170

ctc ggc gct tcc atg gtt                                         608
Leu Gly Ala Ser Met Val
175                 180
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<210> 28
<211> 180
<212> PRT
<213> Corynebacterium glutamicum

<400> 28

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Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser Thr Gly
  1               5                  10                  15

Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp Gln Ser
             20                  25                  30
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Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val Thr Arg
35 40 45

Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr Asp Thr
50 55 60

Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg
65 70 75 80

Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val
85 90 95

Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala Leu Thr
100 105 110

Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser Val Asp
115 120 125

Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val Arg Ile
130 135 140

Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp Gly Thr
145 150 155 160

Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr Leu Gly
165 170 175

Ala Ser Met Val
180

<210> 29
<211> 1230
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1207)
<223> RXA02022

<400> 29
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cttccatcat gttttaacta aggtttgtag gcttaaacct gtg aac tct gaa ctc 115
Val Asn Ser Glu Leu
1 5

aaa cca gga tta gat ctc ctc ggc gac cca att gtc ctt act caa cgt 163
Lys Pro Gly Leu Asp Leu Leu Gly Asp Pro Ile Val Leu Thr Gln Arg
10 15 20

ttg gta gat ata ccg agt ccg tcg ggt cag gaa aag cag att gct gat 211
Leu Val Asp Ile Pro Ser Pro Ser Gly Gln Glu Lys Gln Ile Ala Asp
25 30 35

gaa att gaa gat gcc ctt cgg aac ctt aat cta cct ggt gta gag gtc 259
Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu Pro Gly Val Glu Val
40 45 50

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ttc cgc ttc aac aac aac gtt ctt gct cgc acg aac agg gga ttg gcc    307
Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr Asn Arg Gly Leu Ala
    55                  60                  65

tcg agg gtc atg ctt gct ggt cat atc gat aca gtg ccg atc gcg gac    355
Ser Arg Val Met Leu Ala Gly His Ile Asp Thr Val Pro Ile Ala Asp
 70                  75                  80                  85

aat ctg cca agc cgt gtg gaa gac ggc atc atg tat ggc tgt ggc acc    403
Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met Tyr Gly Cys Gly Thr
                 90                  95                 100

gtc gat atg aaa tct ggg ttg gcg gtg tat ttg cat act ttt gcc acc    451
Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu His Thr Phe Ala Thr
            105                 110                 115

ttg gcc acg tcg act gag ctt aaa cat gat ctg acg ctg att gcg tat    499
Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu Thr Leu Ile Ala Tyr
        120                 125                 130

gag tgc gag gaa gtt gct gat cac ctc aat ggt ttg ggc cac att cgc    547
Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly Leu Gly His Ile Arg
    135                 140                 145

gat gag cat ccg gag tgg ttg gcg gct gat ttg gcg ttg ttg ggt gag    595
Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu Ala Leu Leu Gly Glu
150                 155                 160                 165

cct act ggc ggc tgg att gag gcg ggc tgc cag ggc aat ctg cgc atc    643
Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Gln Gly Asn Leu Arg Ile
                170                 175                 180

aag gtg acg gcg cat ggt gtg cgt gcc cat tcg gcg aga agc tgg ttg    691
Lys Val Thr Ala His Gly Val Arg Ala His Ser Ala Arg Ser Trp Leu
            185                 190                 195

ggt gat aat gcg atg cat aag ttg tcg ccg atc att tcg aag gtt gct    739
Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile Ile Ser Lys Val Ala
        200                 205                 210

gcg tat aag gcc gca gaa gtc aac att gat ggc ttg acc tac cgt gaa    787
Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly Leu Thr Tyr Arg Glu
    215                 220                 225

ggc ctc aac atc gtt ttc tgc gaa tcg ggc gtg gca aac aac gtc att    835
Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val Ala Asn Asn Val Ile
230                 235                 240                 245

cca gac ctc gcg tgg atg aac ctc aac ttc cgt ttc gcg ccg aat cgc    883
Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg Phe Ala Pro Asn Arg
                250                 255                 260

gat ctc aac gag gcg atc gag cat gtc gtc gaa acg ctt gag ctt gac    931
Asp Leu Asn Glu Ala Ile Glu His Val Val Glu Thr Leu Glu Leu Asp
            265                 270                 275

ggt caa gac ggc atc gaa tgg gcc gta gaa gac ggg gca ggc ggt gcc    979
Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp Gly Ala Gly Gly Ala
        280                 285                 290

ctt cca ggc ttg ggg cag cag gtg aca agc ggg ctt atc gac gcc gtc   1027
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Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly Leu Ile Asp Ala Val
    295                 300                 305

ggc cgc gaa aaa atc cgc gca aaa ttc ggc tgg acc gat gtc tca cgt   1075
Gly Arg Glu Lys Ile Arg Ala Lys Phe Gly Trp Thr Asp Val Ser Arg
310                 315                 320                 325

ttt tca gcc atg gga att cca gcc cta aac ttt ggc gct ggt gat cca   1123
Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe Gly Ala Gly Asp Pro
                330                 335                 340

agt ttc gcg cat aaa cgc gac gag cag tgc cca gtg gag caa atc acg   1171
Ser Phe Ala His Lys Arg Asp Glu Gln Cys Pro Val Glu Gln Ile Thr
            345                 350                 355

gat gtg gca gca att ttg aag cag tac ctg agc gag taaccgcatt        1217
Asp Val Ala Ala Ile Leu Lys Gln Tyr Leu Ser Glu
        360                 365

cggggttatc gtg                                                   1230


<210> 30
<211> 369
<212> PRT
<213> Corynebacterium glutamicum

<400> 30
Val Asn Ser Glu Leu Lys Pro Gly Leu Asp Leu Leu Gly Asp Pro Ile
  1               5                  10                  15

Val Leu Thr Gln Arg Leu Val Asp Ile Pro Ser Pro Ser Gly Gln Glu
             20                  25                  30

Lys Gln Ile Ala Asp Glu Ile Glu Asp Ala Leu Arg Asn Leu Asn Leu
         35                  40                  45

Pro Gly Val Glu Val Phe Arg Phe Asn Asn Asn Val Leu Ala Arg Thr
     50                  55                  60

Asn Arg Gly Leu Ala Ser Arg Val Met Leu Ala Gly His Ile Asp Thr
 65                  70                  75                  80

Val Pro Ile Ala Asp Asn Leu Pro Ser Arg Val Glu Asp Gly Ile Met
                 85                  90                  95

Tyr Gly Cys Gly Thr Val Asp Met Lys Ser Gly Leu Ala Val Tyr Leu
            100                 105                 110

His Thr Phe Ala Thr Leu Ala Thr Ser Thr Glu Leu Lys His Asp Leu
        115                 120                 125

Thr Leu Ile Ala Tyr Glu Cys Glu Glu Val Ala Asp His Leu Asn Gly
    130                 135                 140

Leu Gly His Ile Arg Asp Glu His Pro Glu Trp Leu Ala Ala Asp Leu
145                 150                 155                 160

Ala Leu Leu Gly Glu Pro Thr Gly Gly Trp Ile Glu Ala Gly Cys Gln
                165                 170                 175
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Gly Asn Leu Arg Ile Lys Val Thr Ala His Gly Val Arg Ala His Ser
180 185 190

Ala Arg Ser Trp Leu Gly Asp Asn Ala Met His Lys Leu Ser Pro Ile
195 200 205

Ile Ser Lys Val Ala Ala Tyr Lys Ala Ala Glu Val Asn Ile Asp Gly
210 215 220

Leu Thr Tyr Arg Glu Gly Leu Asn Ile Val Phe Cys Glu Ser Gly Val
225 230 235 240

Ala Asn Asn Val Ile Pro Asp Leu Ala Trp Met Asn Leu Asn Phe Arg
245 250 255

Phe Ala Pro Asn Arg Asp Leu Asn Glu Ala Ile Glu His Val Val Glu
260 265 270

Thr Leu Glu Leu Asp Gly Gln Asp Gly Ile Glu Trp Ala Val Glu Asp
275 280 285

Gly Ala Gly Gly Ala Leu Pro Gly Leu Gly Gln Gln Val Thr Ser Gly
290 295 300

Leu Ile Asp Ala Val Gly Arg Glu Lys Ile Arg Ala Lys Phe Gly Trp
305 310 315 320

Thr Asp Val Ser Arg Phe Ser Ala Met Gly Ile Pro Ala Leu Asn Phe
325 330 335

Gly Ala Gly Asp Pro Ser Phe Ala His Lys Arg Asp Glu Gln Cys Pro
340 345 350

Val Glu Gln Ile Thr Asp Val Ala Ala Ile Leu Lys Gln Tyr Leu Ser
355 360 365

Glu

<210> 31
<211> 1059
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1036)
<223> RXA00044

<400> 31
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ttctcacccg cactcgttcc ctcaacccac aaggagcacc atg gct tcc gca act 115
Met Ala Ser Ala Thr
1 5

ttc acc ggc gtg atc cca ccc gta atg acc cca ctc cac gcc gac ggc 163
Phe Thr Gly Val Ile Pro Pro Val Met Thr Pro Leu His Ala Asp Gly
10 15 20

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agt gtg gat gta gaa agc ctc cgc aag ctc gtt gac cac ctc atc aat    211
Ser Val Asp Val Glu Ser Leu Arg Lys Leu Val Asp His Leu Ile Asn
            25                  30                  35

ggt ggc gtc gac gga ctt ttc gca ctg ggc tcc tca ggc gaa gcg gca    259
Gly Gly Val Asp Gly Leu Phe Ala Leu Gly Ser Ser Gly Glu Ala Ala
        40                  45                  50

ttc ctc acc cgc gcc cag cgc aaa ctc gca ctg acc acc atc atc gag    307
Phe Leu Thr Arg Ala Gln Arg Lys Leu Ala Leu Thr Thr Ile Ile Glu
    55                  60                  65

cac acc gca ggc cgc gtt ccc gta act gct ggt gtc att gaa acc acc    355
His Thr Ala Gly Arg Val Pro Val Thr Ala Gly Val Ile Glu Thr Thr
70                  75                  80                  85

act gct cgc gtg att gag ctc gtg gaa gat gcc ctg gag gct ggt gcc    403
Thr Ala Arg Val Ile Glu Leu Val Glu Asp Ala Leu Glu Ala Gly Ala
                90                  95                  100

gaa ggc ctc gtt gcc act gca cct ttc tac acc cgc acc cac gat gtg    451
Glu Gly Leu Val Ala Thr Ala Pro Phe Tyr Thr Arg Thr His Asp Val
            105                 110                 115

gaa att gaa gaa cac ttc cgc aag atc cac gcc gcc gct cca gag ctt    499
Glu Ile Glu Glu His Phe Arg Lys Ile His Ala Ala Ala Pro Glu Leu
        120                 125                 130

cca ctg ttt gcc tac aac atc cca gtg tcg gtg cac tcc aac ctc aac    547
Pro Leu Phe Ala Tyr Asn Ile Pro Val Ser Val His Ser Asn Leu Asn
    135                 140                 145

cca gtc atg ctt ttg acg ctg gcc aag gat ggc gtt ctt gca ggc acc    595
Pro Val Met Leu Leu Thr Leu Ala Lys Asp Gly Val Leu Ala Gly Thr
150                 155                 160                 165

aag gat tcc agt ggc aat gat ggc gca atc cgc tca ctg atc gaa gct    643
Lys Asp Ser Ser Gly Asn Asp Gly Ala Ile Arg Ser Leu Ile Glu Ala
                170                 175                 180

cgt gat gat gct gga ctc act gag cag ttc aag atc ctc acc ggc agc    691
Arg Asp Asp Ala Gly Leu Thr Glu Gln Phe Lys Ile Leu Thr Gly Ser
            185                 190                 195

gaa acc acc gtt gat ttc gcc tac ctt gcg ggt gcc gat gga gtt gtc    739
Glu Thr Thr Val Asp Phe Ala Tyr Leu Ala Gly Ala Asp Gly Val Val
        200                 205                 210

cca ggc ctg ggc aat gtt gat cct gca gca tac gca gct tta gca aaa    787
Pro Gly Leu Gly Asn Val Asp Pro Ala Ala Tyr Ala Ala Leu Ala Lys
    215                 220                 225

ctc tgc ctc gat gga aag tgg gca gaa gct gct gct ttg cag aag cgc    835
Leu Cys Leu Asp Gly Lys Trp Ala Glu Ala Ala Ala Leu Gln Lys Arg
230                 235                 240                 245

atc aac cac ctc ttc cac atc gtc ttc gtg gga gac acc tcc cat atg    883
Ile Asn His Leu Phe His Ile Val Phe Val Gly Asp Thr Ser His Met
                250                 255                 260

tcc gga tcc agc gct ggt ttg ggc ggt ttc aag aca gca ctc gca cac    931
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Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys Thr Ala Leu Ala His
265 270 275

ctt ggc att att gaa tcc aat gcg atg gca gtt cct cac cag agc ctc 979
Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val Pro His Gln Ser Leu
280 285 290

agc gac gaa gaa act gct cgc att cac gcc att gtt gat gaa ttc ctg 1027
Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile Val Asp Glu Phe Leu
295 300 305

tac acc gct taaggcccac acctcatgac tga 1059
Tyr Thr Ala
310

<210> 32
<211> 312
<212> PRT
<213> Corynebacterium glutamicum

<400> 32
Met Ala Ser Ala Thr Phe Thr Gly Val Ile Pro Pro Val Met Thr Pro
1 5 10 15

Leu His Ala Asp Gly Ser Val Asp Val Glu Ser Leu Arg Lys Leu Val
20 25 30

Asp His Leu Ile Asn Gly Gly Val Asp Gly Leu Phe Ala Leu Gly Ser
35 40 45

Ser Gly Glu Ala Ala Phe Leu Thr Arg Ala Gln Arg Lys Leu Ala Leu
50 55 60

Thr Thr Ile Ile Glu His Thr Ala Gly Arg Val Pro Val Thr Ala Gly
65 70 75 80

Val Ile Glu Thr Thr Thr Ala Arg Val Ile Glu Leu Val Glu Asp Ala
85 90 95

Leu Glu Ala Gly Ala Glu Gly Leu Val Ala Thr Ala Pro Phe Tyr Thr
100 105 110

Arg Thr His Asp Val Glu Ile Glu Glu His Phe Arg Lys Ile His Ala
115 120 125

Ala Ala Pro Glu Leu Pro Leu Phe Ala Tyr Asn Ile Pro Val Ser Val
130 135 140

His Ser Asn Leu Asn Pro Val Met Leu Leu Thr Leu Ala Lys Asp Gly
145 150 155 160

Val Leu Ala Gly Thr Lys Asp Ser Ser Gly Asn Asp Gly Ala Ile Arg
165 170 175

Ser Leu Ile Glu Ala Arg Asp Asp Ala Gly Leu Thr Glu Gln Phe Lys
180 185 190

Ile Leu Thr Gly Ser Glu Thr Thr Val Asp Phe Ala Tyr Leu Ala Gly
195 200 205

Ala Asp Gly Val Val Pro Gly Leu Gly Asn Val Asp Pro Ala Ala Tyr
210 215 220

Ala Ala Leu Ala Lys Leu Cys Leu Asp Gly Lys Trp Ala Glu Ala Ala
225 230 235 240

Ala Leu Gln Lys Arg Ile Asn His Leu Phe His Ile Val Phe Val Gly
245 250 255

Asp Thr Ser His Met Ser Gly Ser Ser Ala Gly Leu Gly Gly Phe Lys
260 265 270

Thr Ala Leu Ala His Leu Gly Ile Ile Glu Ser Asn Ala Met Ala Val
275 280 285

Pro His Gln Ser Leu Ser Asp Glu Glu Thr Ala Arg Ile His Ala Ile
290 295 300

Val Asp Glu Phe Leu Tyr Thr Ala
305 310

<210> 33
<211> 867
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(844)
<223> RXA00863

<400> 33
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gtttgaaaaa ctcttcgccc cacgaaaatg aaggagcata atg gga atc aag gtt 115
Met Gly Ile Lys Val
1 5

ggc gtt ctc gga gcc aaa ggc cgt gtt ggt caa act att gtg gca gca 163
Gly Val Leu Gly Ala Lys Gly Arg Val Gly Gln Thr Ile Val Ala Ala
10 15 20

gtc aat gag tcc gac gat ctg gag ctt gtt gca gag atc ggc gtc gac 211
Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala Glu Ile Gly Val Asp
25 30 35

gat gat ttg agc ctt ctg gta gac aac ggc gct gaa gtt gtc gtt gac 259
Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala Glu Val Val Val Asp
40 45 50

ttc acc act cct aac gct gtg atg ggc aac ctg gag ttc tgc atc aac 307
Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu Glu Phe Cys Ile Asn
55 60 65

aac ggc att tct gcg gtt gtt gga acc acg ggc ttc gat gat gct cgt 355
Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly Phe Asp Asp Ala Arg
70 75 80 85

ttg gag cag gtt cgc gac tgg ctt gaa gga aaa gac aat gtc ggt gtt 403
Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys Asp Asn Val Gly Val

90 95 100

ctg atc gca cct aac ttt gct atc tct gcg gtg ttg acc atg gtc ttt 451
Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val Leu Thr Met Val Phe
105 110 115

tcc aag cag gct gcc cgc ttc ttc gaa tca gct gaa gtt att gag ctg 499
Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala Glu Val Ile Glu Leu
120 125 130

cac cac ccc aac aag ctg gat gca cct tca ggc acc gcg atc cac act 547
His His Pro Asn Lys Leu Asp Ala Pro Ser Gly Thr Ala Ile His Thr
135 140 145

gct cag ggc att gct gcg gca cgc aaa gaa gca ggc atg gac gca cag 595
Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala Gly Met Asp Ala Gln
150 155 160 165

cca gat gcg acc gag cag gca ctt gag ggt tcc cgt ggc gca agc gta 643
Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser Arg Gly Ala Ser Val
170 175 180

gat gga atc ccg gtt cat gca gtc cgc atg tcc ggc atg gtt gct cac 691
Asp Gly Ile Pro Val His Ala Val Arg Met Ser Gly Met Val Ala His
185 190 195

gag caa gtt atc ttt ggc acc cag ggt cag acc ttg acc atc aag cag 739
Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr Leu Thr Ile Lys Gln
200 205 210

gac tcc tat gat cgc aac tca ttt gca cca ggt gtc ttg gtg ggt gtg 787
Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly Val Leu Val Gly Val
215 220 225

cgc aac att gca cag cac cca ggc cta gtc gta gga ctt gag cat tac 835
Arg Asn Ile Ala Gln His Pro Gly Leu Val Val Gly Leu Glu His Tyr
230 235 240 245

cta ggc ctg taaaggctca tttcagcagc ggg 867
Leu Gly Leu

<210> 34
<211> 248
<212> PRT
<213> Corynebacterium glutamicum

<400> 34
Met Gly Ile Lys Val Gly Val Leu Gly Ala Lys Gly Arg Val Gly Gln
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Thr Ile Val Ala Ala Val Asn Glu Ser Asp Asp Leu Glu Leu Val Ala
20 25 30

Glu Ile Gly Val Asp Asp Asp Leu Ser Leu Leu Val Asp Asn Gly Ala
35 40 45

Glu Val Val Val Asp Phe Thr Thr Pro Asn Ala Val Met Gly Asn Leu
50 55 60

Glu Phe Cys Ile Asn Asn Gly Ile Ser Ala Val Val Gly Thr Thr Gly
65 70 75 80

Phe Asp Asp Ala Arg Leu Glu Gln Val Arg Asp Trp Leu Glu Gly Lys
85 90 95

Asp Asn Val Gly Val Leu Ile Ala Pro Asn Phe Ala Ile Ser Ala Val
100 105 110

Leu Thr Met Val Phe Ser Lys Gln Ala Ala Arg Phe Phe Glu Ser Ala
115 120 125

Glu Val Ile Glu Leu His His Pro Asn Lys Leu Asp Ala Pro Ser Gly
130 135 140

Thr Ala Ile His Thr Ala Gln Gly Ile Ala Ala Ala Arg Lys Glu Ala
145 150 155 160

Gly Met Asp Ala Gln Pro Asp Ala Thr Glu Gln Ala Leu Glu Gly Ser
165 170 175

Arg Gly Ala Ser Val Asp Gly Ile Pro Val His Ala Val Arg Met Ser
180 185 190

Gly Met Val Ala His Glu Gln Val Ile Phe Gly Thr Gln Gly Gln Thr
195 200 205

Leu Thr Ile Lys Gln Asp Ser Tyr Asp Arg Asn Ser Phe Ala Pro Gly
210 215 220

Val Leu Val Gly Val Arg Asn Ile Ala Gln His Pro Gly Leu Val Val
225 230 235 240

Gly Leu Glu His Tyr Leu Gly Leu
245

<210> 35
<211> 873
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(850)
<223> RXA00864

<400> 35
acagcaccca ggcctagtcg taggacttga gcattaccta ggcctgtaaa ggctcatttc 60

agcagcgggt ggaattttt aaaaggagcg tttaaaggct gtg gcc gaa caa gtt 115
Val Ala Glu Gln Val
1 5

aaa ttg agc gtg gag ttg ata gcg tgc agt tct ttt act cca ccc gct 163
Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser Phe Thr Pro Pro Ala
10 15 20

gat gtt gag tgg tca act gat gtt gag ggc gcg gaa gca ctc gtc gag 211
Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala Glu Ala Leu Val Glu
25 30 35

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ttt gcg ggt cgt gcc tgc tac gaa act ttt gat aag ccg aac cct cga   259
Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp Lys Pro Asn Pro Arg
         40                  45                  50

act gct tcc aat gct gcg tat ctg cgc cac atc atg gaa gtg ggg cac   307
Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile Met Glu Val Gly His
     55                  60                  65

act gct ttg ctt gag cat gcc aat gcc acg atg tat atc cga ggc att   355
Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met Tyr Ile Arg Gly Ile
 70                  75                  80                  85

tct cgg tcc gcg acc cat gaa ttg gtc cga cac cgc cat ttt tcc ttc   403
Ser Arg Ser Ala Thr His Glu Leu Val Arg His Arg His Phe Ser Phe
                 90                  95                 100

tct caa ctg tct cag cgt ttc gtg cac agc gga gaa tcg gaa gta gtg   451
Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly Glu Ser Glu Val Val
            105                 110                 115

gtg ccc act ctc atc gat gaa gat ccg cag ttg cgt gaa ctt ttc atg   499
Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu Arg Glu Leu Phe Met
        120                 125                 130

cac gcc atg gat gag tct cgg ttc gct ttc aat gag ctg ctt aat gcg   547
His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn Glu Leu Leu Asn Ala
    135                 140                 145

ctg gaa gaa aaa ctt ggc gat gaa ccg aat gca ctt tta agg aaa aag   595
Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala Leu Leu Arg Lys Lys
150                 155                 160                 165

cag gct cgt caa gca gct cgc gct gtg ctg ccc aac gct aca gag tcc   643
Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro Asn Ala Thr Glu Ser
                170                 175                 180

aga atc gtg gtg tct gga aac ttc cgc acc tgg agg cat ttc att ggc   691
Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp Arg His Phe Ile Gly
            185                 190                 195

atg cga gcc agt gaa cat gca gac gtc gaa atc cgc gaa gta gcg gta   739
Met Arg Ala Ser Glu His Ala Asp Val Glu Ile Arg Glu Val Ala Val
        200                 205                 210

gaa tgt tta aga aag ctg cag gta gca gcg cca act gtt ttc ggt gat   787
Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro Thr Val Phe Gly Asp
    215                 220                 225

ttt gag att gaa act ttg gca gac gga tcg caa atg gca aca agc ccg   835
Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln Met Ala Thr Ser Pro
230                 235                 240                 245

tat gtc atg gac ttt taacgcaaag ctcacaccca cga                    873
Tyr Val Met Asp Phe
                250
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<210> 36
<211> 250
<212> PRT

<213> Corynebacterium glutamicum

<400> 36

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Val Ala Glu Gln Val Lys Leu Ser Val Glu Leu Ile Ala Cys Ser Ser
  1               5                  10                  15

Phe Thr Pro Pro Ala Asp Val Glu Trp Ser Thr Asp Val Glu Gly Ala
             20                  25                  30

Glu Ala Leu Val Glu Phe Ala Gly Arg Ala Cys Tyr Glu Thr Phe Asp
         35                  40                  45

Lys Pro Asn Pro Arg Thr Ala Ser Asn Ala Ala Tyr Leu Arg His Ile
     50                  55                  60

Met Glu Val Gly His Thr Ala Leu Leu Glu His Ala Asn Ala Thr Met
 65                  70                  75                  80

Tyr Ile Arg Gly Ile Ser Arg Ser Ala Thr His Glu Leu Val Arg His
                 85                  90                  95

Arg His Phe Ser Phe Ser Gln Leu Ser Gln Arg Phe Val His Ser Gly
            100                 105                 110

Glu Ser Glu Val Val Val Pro Thr Leu Ile Asp Glu Asp Pro Gln Leu
        115                 120                 125

Arg Glu Leu Phe Met His Ala Met Asp Glu Ser Arg Phe Ala Phe Asn
    130                 135                 140

Glu Leu Leu Asn Ala Leu Glu Glu Lys Leu Gly Asp Glu Pro Asn Ala
145                 150                 155                 160

Leu Leu Arg Lys Lys Gln Ala Arg Gln Ala Ala Arg Ala Val Leu Pro
                165                 170                 175

Asn Ala Thr Glu Ser Arg Ile Val Val Ser Gly Asn Phe Arg Thr Trp
            180                 185                 190

Arg His Phe Ile Gly Met Arg Ala Ser Glu His Ala Asp Val Glu Ile
        195                 200                 205

Arg Glu Val Ala Val Glu Cys Leu Arg Lys Leu Gln Val Ala Ala Pro
    210                 215                 220

Thr Val Phe Gly Asp Phe Glu Ile Glu Thr Leu Ala Asp Gly Ser Gln
225                 230                 235                 240

Met Ala Thr Ser Pro Tyr Val Met Asp Phe
                245                 250
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<210> 37
<211> 608
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (69)..(608)
<223> RXA02843

<400> 37
cccattgcgc ggaggtcgca ccccttccga cttgaactga taggccgata gaaattattc 60

tggacgtc atg act act gct tcc gca acc gga att gca aca ctg acc tcc 110
Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser
1 5 10

acc ggc gac gtc ctg gac gtg tgg tat cca gaa atc ggg tcc acc gac 158
Thr Gly Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp
15 20 25 30

cag tcc gcg ctc aca cct cta gaa ggc gtc gat gaa gat cga aac gtc 206
Gln Ser Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val
35 40 45

acc cgc aaa atc gtg acg aca act atc gac acc gac gca gcc ccc acc 254
Thr Arg Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr
50 55 60

gac acc tac gat gca tgg ctg cgc ctt cac ctc ctc tcc cac cgc gtt 302
Asp Thr Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val
65 70 75

ttc cgc cct cac acc atc aac cta gac ggc att ttc ggc ctc ctc aac 350
Phe Arg Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn
80 85 90

aat gtc gtg tgg acc aac ttc gga ccg tgc gca gtt gac ggt ttc gca 398
Asn Val Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala
95 100 105 110

ctc acc cgc gcg cgc ctg tca cgc cga ggc caa gtt acg gtt tat agc 446
Leu Thr Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser
115 120 125

gtc gac aag ttc cca cgc atg gtc gac tat gtg gtt ccc tcg ggc gtg 494
Val Asp Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val
130 135 140

cgc atc ggt gac gcc gac cgc gtc cga ctt ggc gcg tac ctg gca gat 542
Arg Ile Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp
145 150 155

ggc acc acc gtg atg cat gag ggc ttc gtg aac ttc aac gct ggc acg 590
Gly Thr Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr
160 165 170

ctc ggc gct tcc atg gtt 608
Leu Gly Ala Ser Met Val
175 180

<210> 38
<211> 180
<212> PRT
<213> Corynebacterium glutamicum

<400> 38
Met Thr Thr Ala Ser Ala Thr Gly Ile Ala Thr Leu Thr Ser Thr Gly
1 5 10 15

Asp Val Leu Asp Val Trp Tyr Pro Glu Ile Gly Ser Thr Asp Gln Ser
20 25 30

Ala Leu Thr Pro Leu Glu Gly Val Asp Glu Asp Arg Asn Val Thr Arg
35 40 45

Lys Ile Val Thr Thr Thr Ile Asp Thr Asp Ala Ala Pro Thr Asp Thr
50 55 60

Tyr Asp Ala Trp Leu Arg Leu His Leu Leu Ser His Arg Val Phe Arg
65 70 75 80

Pro His Thr Ile Asn Leu Asp Gly Ile Phe Gly Leu Leu Asn Asn Val
85 90 95

Val Trp Thr Asn Phe Gly Pro Cys Ala Val Asp Gly Phe Ala Leu Thr
100 105 110

Arg Ala Arg Leu Ser Arg Arg Gly Gln Val Thr Val Tyr Ser Val Asp
115 120 125

Lys Phe Pro Arg Met Val Asp Tyr Val Val Pro Ser Gly Val Arg Ile
130 135 140

Gly Asp Ala Asp Arg Val Arg Leu Gly Ala Tyr Leu Ala Asp Gly Thr
145 150 155 160

Thr Val Met His Glu Gly Phe Val Asn Phe Asn Ala Gly Thr Leu Gly
165 170 175

Ala Ser Met Val
180

<210> 39
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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1120)
<223> RXN00355

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ggtcctgatg aaagagatgt ccctgaatca tcatctaagt atg cat ctc ggt aag 115
Met His Leu Gly Lys
1 5

ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163
Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met
10 15 20

acc aac atc cgc gta gct atc gtg ggc tac gga aac ctg gga cgc agc 211
Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser
25 30 35

gtc gaa aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc 259

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Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met Asp Leu Val Gly Ile
        40                  45                  50

ttc tcg cgc cgg gcc acc ctc gac aca aag acg cca gtc ttt gat gtc    307
Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr Pro Val Phe Asp Val
    55                  60                  65

gcc gac gtg gac aag cac gcc gac gac gtg gac gtg ctg ttc ctg tgc    355
Ala Asp Val Asp Lys His Ala Asp Asp Val Asp Val Leu Phe Leu Cys
70                  75                  80                  85

atg ggc tcc gcc acc gac atc cct gag cag gca cca aag ttc gcg cag    403
Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala Pro Lys Phe Ala Gln
                90                  95                  100

ttc gcc tgc acc gta gac acc tac gac aac cac cgc gac atc cca cgc    451
Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His Arg Asp Ile Pro Arg
            105                 110                 115

cac cgc cag gtc atg aac gaa gcc gcc acc gca gcc ggc aac gtt gca    499
His Arg Gln Val Met Asn Glu Ala Ala Thr Ala Ala Gly Asn Val Ala
        120                 125                 130

ctg gtc tct acc ggc tgg gat cca gga atg ttc tcc atc aac cgc gtc    547
Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe Ser Ile Asn Arg Val
    135                 140                 145

tac gca gcg gca gtc tta gcc gag cac cag cag cac acc ttc tgg ggc    595
Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln His Thr Phe Trp Gly
150                 155                 160                 165

cca ggt ttg tca cag ggc cac tcc gat gct ttg cga cgc atc cct ggc    643
Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu Arg Arg Ile Pro Gly
                170                 175                 180

gtt caa aag gca gtc cag tac acc ctc cca tcc gaa gac gcc ctg gaa    691
Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser Glu Asp Ala Leu Glu
            185                 190                 195

aag gcc cgc cgc ggc gaa gcc ggc gac ctt acc gga aag caa acc cac    739
Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr Gly Lys Gln Thr His
        200                 205                 210

aag cgc caa tgc ttc gtg gtt gcc gac gcg gcc gat cac gag cgc atc    787
Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala Asp His Glu Arg Ile
    215                 220                 225

gaa aac gac atc cgc acc atg cct gat tac ttc gtt ggc tac gaa gtc    835
Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe Val Gly Tyr Glu Val
230                 235                 240                 245

gaa gtc aac ttc atc gac gaa gca acc ttc gac tcc gag cac acc ggc    883
Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp Ser Glu His Thr Gly
                250                 255                 260

atg cca cac ggt ggc cac gtg att acc acc ggc gac acc ggt ggc ttc    931
Met Pro His Gly Gly His Val Ile Thr Thr Gly Asp Thr Gly Gly Phe
            265                 270                 275

aac cac acc gtg gaa tac atc ctc aag ctg gac cga aac cca gat ttc    979
Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp Arg Asn Pro Asp Phe
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        280                 285                 290

acc gct tcc tca cag atc gct ttc ggt cgc gca gct cac cgc atg aag    1027
Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala Ala His Arg Met Lys
    295                 300                 305

cag cag ggc caa agc gga gct ttc acc gtc ctc gaa gtt gct cca tac    1075
Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu Glu Val Ala Pro Tyr
310                 315                 320                 325

ctg ctc tcc cca gag aac ttg gac gat ctg atc gca cgc gac gtc        1120
Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile Ala Arg Asp Val
                330                 335                 340

taatttagct cgaggggcaa gga                                          1143


<210> 40
<211> 340
<212> PRT
<213> Corynebacterium glutamicum

<400> 40
Met His Leu Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu
  1               5                  10                  15

Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly
             20                  25                  30

Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met
         35                  40                  45

Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr
     50                  55                  60

Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp
 65                  70                  75                  80

Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala
                 85                  90                  95

Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His
            100                 105                 110

Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala
        115                 120                 125

Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe
    130                 135                 140

Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln
145                 150                 155                 160

His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu
                165                 170                 175

Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser
            180                 185                 190

Glu Asp Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr
        195                 200                 205
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Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala
    210   215   220

Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe
225   230   235   240

Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp
                245   250   255

Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly
            260   265   270

Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys Leu Asp
        275   280   285

Arg Asn Pro Asp Phe Thr Ala Ser Ser Gln Ile Ala Phe Gly Arg Ala
    290   295   300

Ala His Arg Met Lys Gln Gln Gly Gln Ser Gly Ala Phe Thr Val Leu
305   310   315   320

Glu Val Ala Pro Tyr Leu Leu Ser Pro Glu Asn Leu Asp Asp Leu Ile
                325   330   335

Ala Arg Asp Val
            340

<210> 41
<211> 958
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(958)
<223> FRXA00352

<400> 41
aatagatcag cgcatccgtg gtggaaccaa aaggctcaac aatacgaaac gttcgctttc 60

ggtcctgatg aaagagatgt ccctgaatca tcatctaagt atg cat ctc ggt aag 115
Met His Leu Gly Lys
1   5

ctc gac cag gac agt gcc acc aca att ttg gag gat tac aag aac atg 163
Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu Asp Tyr Lys Asn Met
            10   15   20

acc aac atc cgc gta gct atc gtg ggc tac gga aac ctg gga cgc agc 211
Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly Asn Leu Gly Arg Ser
        25   30   35

gtc gaa aag ctt att gcc aag cag ccc gac atg gac ctt gta gga atc 259
Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met Asp Leu Val Gly Ile
    40   45   50

ttc tcg cgc cgg gcc acc ctc gac aca aag acg cca gtc ttt gat gtc 307
Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr Pro Val Phe Asp Val
    55   60   65

```
gcc gac gtg gac aag cac gcc gac gac gtg gac gtg ctg ttc ctg tgc   355
Ala Asp Val Asp Lys His Ala Asp Asp Val Asp Val Leu Phe Leu Cys
 70                  75                  80                  85

atg ggc tcc gcc acc gac atc cct gag cag gca cca aag ttc gcg cag   403
Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala Pro Lys Phe Ala Gln
                90                  95                 100

ttc gcc tgc acc gta gac acc tac gac aac cac cgc gac atc cca cgc   451
Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His Arg Asp Ile Pro Arg
            105                 110                 115

cac cgc cag gtc atg aac gaa gcc gcc acc gca gcc ggc aac gtt gca   499
His Arg Gln Val Met Asn Glu Ala Ala Thr Ala Ala Gly Asn Val Ala
        120                 125                 130

ctg gtc tct acc ggc tgg gat cca gga atg ttc tcc atc aac cgc gtc   547
Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe Ser Ile Asn Arg Val
    135                 140                 145

tac gca gcg gca gtc tta gcc gag cac cag cag cac acc ttc tgg ggc   595
Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln His Thr Phe Trp Gly
150                 155                 160                 165

cca ggt ttg tca cag ggc cac tcc gat gct ttg cga cgc atc cct ggc   643
Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu Arg Arg Ile Pro Gly
                170                 175                 180

gtt caa aag gca gtc cag tac acc ctc cca tcc gaa gac gcc ctg gaa   691
Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser Glu Asp Ala Leu Glu
            185                 190                 195

aag gcc cgc cgc ggc gaa gcc ggc gac ctt acc gga aag caa acc cac   739
Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr Gly Lys Gln Thr His
        200                 205                 210

aag cgc caa tgc ttc gtg gtt gcc gac gcg gcc gat cac gag cgc atc   787
Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala Asp His Glu Arg Ile
    215                 220                 225

gaa aac gac atc cgc acc atg cct gat tac ttc gtt ggc tac gaa gtc   835
Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe Val Gly Tyr Glu Val
230                 235                 240                 245

gaa gtc aac ttc atc gac gaa gca acc ttc gac tcc gag cac acc ggc   883
Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp Ser Glu His Thr Gly
                250                 255                 260

atg cca cac ggt ggc cac gtg att acc acc ggc gac acc ggt ggc ttc   931
Met Pro His Gly Gly His Val Ile Thr Thr Gly Asp Thr Gly Gly Phe
            265                 270                 275

aac cac acc gtg gaa tac atc ctc aag                              958
Asn His Thr Val Glu Tyr Ile Leu Lys
        280                 285
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<210> 42
<211> 286
<212> PRT

<213> Corynebacterium glutamicum

<400> 42

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Met His Leu Gly Lys Leu Asp Gln Asp Ser Ala Thr Thr Ile Leu Glu
 1               5                  10                  15

Asp Tyr Lys Asn Met Thr Asn Ile Arg Val Ala Ile Val Gly Tyr Gly
            20                  25                  30

Asn Leu Gly Arg Ser Val Glu Lys Leu Ile Ala Lys Gln Pro Asp Met
        35                  40                  45

Asp Leu Val Gly Ile Phe Ser Arg Arg Ala Thr Leu Asp Thr Lys Thr
    50                  55                  60

Pro Val Phe Asp Val Ala Asp Val Asp Lys His Ala Asp Asp Val Asp
65                  70                  75                  80

Val Leu Phe Leu Cys Met Gly Ser Ala Thr Asp Ile Pro Glu Gln Ala
                85                  90                  95

Pro Lys Phe Ala Gln Phe Ala Cys Thr Val Asp Thr Tyr Asp Asn His
            100                 105                 110

Arg Asp Ile Pro Arg His Arg Gln Val Met Asn Glu Ala Ala Thr Ala
        115                 120                 125

Ala Gly Asn Val Ala Leu Val Ser Thr Gly Trp Asp Pro Gly Met Phe
    130                 135                 140

Ser Ile Asn Arg Val Tyr Ala Ala Ala Val Leu Ala Glu His Gln Gln
145                 150                 155                 160

His Thr Phe Trp Gly Pro Gly Leu Ser Gln Gly His Ser Asp Ala Leu
                165                 170                 175

Arg Arg Ile Pro Gly Val Gln Lys Ala Val Gln Tyr Thr Leu Pro Ser
            180                 185                 190

Glu Asp Ala Leu Glu Lys Ala Arg Arg Gly Glu Ala Gly Asp Leu Thr
        195                 200                 205

Gly Lys Gln Thr His Lys Arg Gln Cys Phe Val Val Ala Asp Ala Ala
    210                 215                 220

Asp His Glu Arg Ile Glu Asn Asp Ile Arg Thr Met Pro Asp Tyr Phe
225                 230                 235                 240

Val Gly Tyr Glu Val Glu Val Asn Phe Ile Asp Glu Ala Thr Phe Asp
                245                 250                 255

Ser Glu His Thr Gly Met Pro His Gly Gly His Val Ile Thr Thr Gly
            260                 265                 270

Asp Thr Gly Gly Phe Asn His Thr Val Glu Tyr Ile Leu Lys
        275                 280                 285
```

<210> 43
<211> 1400
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1377)
<223> RXA00972

<400> 43

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cct gca cct ggt tgg cgt ttc cgc acc gga gaa gat gta aca atg gct   48
Pro Ala Pro Gly Trp Arg Phe Arg Thr Gly Glu Asp Val Thr Met Ala
  1               5                  10                  15

aca gtt gaa aat ttc aat gaa ctt ccc gca cac gta tgg cca cgc aat   96
Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro Arg Asn
             20                  25                  30

gcc gtg cgc caa gaa gac ggc gtt gtc acc gtc gct ggt gtg cct ctg   144
Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu
         35                  40                  45

cct gac ctc gct gaa gaa tac gga acc cca ctg ttc gta gtc gac gag   192
Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu
     50                  55                  60

gac gat ttc cgt tcc cgc tgt cgc gac atg gct acc gca ttc ggt gga   240
Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly
 65                  70                  75                  80

cca ggc aat gtg cac tac gca tct aaa gcg ttc ctg acc aag acc att   288
Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile
                 85                  90                  95

gca cgt tgg gtt gat gaa gag ggg ctg gca ctg gac att gca tcc atc   336
Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile
            100                 105                 110

aac gaa ctg ggc att gcc ctg gcc gct ggt ttc ccc gcc agc cgt atc   384
Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile
        115                 120                 125

acc gcg cac ggc aac aac aaa ggc gta gag ttc ctg cgc gcg ttg gtt   432
Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val
    130                 135                 140

caa aac ggt gtg gga cac gtg gtg ctg gac tcc gca cag gaa cta gaa   480
Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu
145                 150                 155                 160

ctg ttg gat tac gtt gcc gct ggt gaa ggc aag att cag gac gtg ttg   528
Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu
                165                 170                 175

atc cgc gta aag cca ggc atc gaa gca cac acc cac gag ttc atc gcc   576
Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe Ile Ala
            180                 185                 190

act agc cac gaa gac cag aag ttc gga ttc tcc ctg gca tcc ggt tcc   624
Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser
        195                 200                 205

gca ttc gaa gca gca aaa gcc gcc aac aac gca gaa aac ctg aac ctg   672
```

```
Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu Asn Leu
    210                 215                 220

gtt ggc ctg cac tgc cac gtt ggt tcc cag gtg ttc gac gcc gaa ggc     720
Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Glu Gly
225                 230                 235                 240

ttc aag ctg gca gca gaa cgc gtg ttg ggc ctg tac tca cag atc cac     768
Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln Ile His
                245                 250                 255

agc gaa ctg ggc gtt gcc ctt cct gaa ctg gat ctc ggt ggc gga tac     816
Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr
            260                 265                 270

ggc att gcc tat acc gca gct gaa gaa cca ctc aac gtc gca gaa gtt     864
Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala Glu Val
        275                 280                 285

gcc tcc gac ctg ctc acc gca gtc gga aaa atg gca gcg gaa cta ggc     912
Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu Leu Gly
    290                 295                 300

atc gac gca cca acc gtg ctt gtt gag ccc ggc cgc gct atc gca ggc     960
Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly
305                 310                 315                 320

ccc tcc acc gtg acc atc tac gaa gtc ggc acc acc aaa gac gtc cac    1008
Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp Val His
                325                 330                 335

gta gac gac gac aaa acc cgc cgt tac atc gcc gtg gac gga ggc atg    1056
Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly Gly Met
            340                 345                 350

tcc gac aac atc cgc cca gca ctc tac ggg tcc gaa tac gac gcc cgc    1104
Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp Ala Arg
        355                 360                 365

gta gta tcc cgc ttc gcc gaa gga gac cca gta agc acc cgc atc gtg    1152
Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg Ile Val
    370                 375                 380

ggc tcc cac tgc gaa tcc ggc gat atc ctg atc aac gat gaa atc tac    1200
Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu Ile Tyr
385                 390                 395                 400

cca tct gac atc acc agc ggc gac ttc ctt gca ctc gca gcc acc ggc    1248
Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala Thr Gly
                405                 410                 415

gca tac tgc tac gcc atg agc tcc cgc tac aac gcc ttc aca cgg ccc    1296
Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr Arg Pro
            420                 425                 430

gcc gtc gtg tcc gtc cgc gct ggc agc tcc cgc ctc atg ctg cgc cgc    1344
Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu Arg Arg
        435                 440                 445

gaa acg ctc gac gac atc ctc tca cta gag gca taacgctttt cgacgcctga 1397
Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala
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450 455

ccc 1400

<210> 44
<211> 459
<212> PRT
<213> Corynebacterium glutamicum

<400> 44
Pro Ala Pro Gly Trp Arg Phe Arg Thr Gly Glu Asp Val Thr Met Ala
1 5 10 15

Thr Val Glu Asn Phe Asn Glu Leu Pro Ala His Val Trp Pro Arg Asn
20 25 30

Ala Val Arg Gln Glu Asp Gly Val Val Thr Val Ala Gly Val Pro Leu
35 40 45

Pro Asp Leu Ala Glu Glu Tyr Gly Thr Pro Leu Phe Val Val Asp Glu
50 55 60

Asp Asp Phe Arg Ser Arg Cys Arg Asp Met Ala Thr Ala Phe Gly Gly
65 70 75 80

Pro Gly Asn Val His Tyr Ala Ser Lys Ala Phe Leu Thr Lys Thr Ile
85 90 95

Ala Arg Trp Val Asp Glu Glu Gly Leu Ala Leu Asp Ile Ala Ser Ile
100 105 110

Asn Glu Leu Gly Ile Ala Leu Ala Ala Gly Phe Pro Ala Ser Arg Ile
115 120 125

Thr Ala His Gly Asn Asn Lys Gly Val Glu Phe Leu Arg Ala Leu Val
130 135 140

Gln Asn Gly Val Gly His Val Val Leu Asp Ser Ala Gln Glu Leu Glu
145 150 155 160

Leu Leu Asp Tyr Val Ala Ala Gly Glu Gly Lys Ile Gln Asp Val Leu
165 170 175

Ile Arg Val Lys Pro Gly Ile Glu Ala His Thr His Glu Phe Ile Ala
180 185 190

Thr Ser His Glu Asp Gln Lys Phe Gly Phe Ser Leu Ala Ser Gly Ser
195 200 205

Ala Phe Glu Ala Ala Lys Ala Ala Asn Asn Ala Glu Asn Leu Asn Leu
210 215 220

Val Gly Leu His Cys His Val Gly Ser Gln Val Phe Asp Ala Glu Gly
225 230 235 240

Phe Lys Leu Ala Ala Glu Arg Val Leu Gly Leu Tyr Ser Gln Ile His
245 250 255

Ser Glu Leu Gly Val Ala Leu Pro Glu Leu Asp Leu Gly Gly Gly Tyr
260 265 270

```
Gly Ile Ala Tyr Thr Ala Ala Glu Glu Pro Leu Asn Val Ala Glu Val
        275                 280                 285

Ala Ser Asp Leu Leu Thr Ala Val Gly Lys Met Ala Ala Glu Leu Gly
    290                 295                 300

Ile Asp Ala Pro Thr Val Leu Val Glu Pro Gly Arg Ala Ile Ala Gly
305                 310                 315                 320

Pro Ser Thr Val Thr Ile Tyr Glu Val Gly Thr Thr Lys Asp Val His
                325                 330                 335

Val Asp Asp Asp Lys Thr Arg Arg Tyr Ile Ala Val Asp Gly Gly Met
            340                 345                 350

Ser Asp Asn Ile Arg Pro Ala Leu Tyr Gly Ser Glu Tyr Asp Ala Arg
        355                 360                 365

Val Val Ser Arg Phe Ala Glu Gly Asp Pro Val Ser Thr Arg Ile Val
    370                 375                 380

Gly Ser His Cys Glu Ser Gly Asp Ile Leu Ile Asn Asp Glu Ile Tyr
385                 390                 395                 400

Pro Ser Asp Ile Thr Ser Gly Asp Phe Leu Ala Leu Ala Ala Thr Gly
                405                 410                 415

Ala Tyr Cys Tyr Ala Met Ser Ser Arg Tyr Asn Ala Phe Thr Arg Pro
            420                 425                 430

Ala Val Val Ser Val Arg Ala Gly Ser Ser Arg Leu Met Leu Arg Arg
        435                 440                 445

Glu Thr Leu Asp Asp Ile Leu Ser Leu Glu Ala
    450                 455


<210> 45
<211> 2121
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2098)
<223> RXA02653

<400> 45
agacagagtg ttagtgcgtg gggcagctct cactttcatc gacatcactc gagtatgctc 60

accggccgta ttcattccaa taacccgcac agggaaacta atg ata ccg aag ccc   115
                                            Met Ile Pro Lys Pro
                                              1               5

gac gtg acc gac tta tat tta gag gac ctc tta aat gag ggt tcg gaa   163
Asp Val Thr Asp Leu Tyr Leu Glu Asp Leu Leu Asn Glu Gly Ser Glu
                  10                  15                  20

aag att cgg tcc gcc aag gat ctt tcc gaa ctt agg aca gtt cta aaa   211
Lys Ile Arg Ser Ala Lys Asp Leu Ser Glu Leu Arg Thr Val Leu Lys
```

```
                25                  30                  35

gag gtt tcc tcc caa att cag gaa cga gct ggg aaa aaa gat gaa gaa      259
Glu Val Ser Ser Gln Ile Gln Glu Arg Ala Gly Lys Lys Asp Glu Glu
            40                  45                  50

tgg gga atg ggg gcc act tgg cgg gag ctg tac ccc agc atc gtg gaa      307
Trp Gly Met Gly Ala Thr Trp Arg Glu Leu Tyr Pro Ser Ile Val Glu
        55                  60                  65

cgc gct tcc tac gaa ggg cgt gac agc cta atc gga ttt gat cac tta      355
Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile Gly Phe Asp His Leu
 70                  75                  80                  85

gcc cgg gaa atg gaa aga tta gcc ttc ggc cca cca tcc gaa agt ttt      403
Ala Arg Glu Met Glu Arg Leu Ala Phe Gly Pro Pro Ser Glu Ser Phe
                 90                  95                 100

gaa tac ctc caa gaa ctc gta aaa tcc gga gtg gta gac atc act cac      451
Glu Tyr Leu Gln Glu Leu Val Lys Ser Gly Val Val Asp Ile Thr His
            105                 110                 115

ctg cat cgt ggc cgg gaa cca ctg aca gat tta gtt cgt gaa ctt gaa      499
Leu His Arg Gly Arg Glu Pro Leu Thr Asp Leu Val Arg Glu Leu Glu
        120                 125                 130

ata act gtg gtg ata gac gct gtt ctt ccc ccg ccg gga gta gtg cca      547
Ile Thr Val Val Ile Asp Ala Val Leu Pro Pro Pro Gly Val Val Pro
    135                 140                 145

ggc aca ttg gtg cac aat ttg gta aaa gag gga tat gcc aga atg cgt      595
Gly Thr Leu Val His Asn Leu Val Lys Glu Gly Tyr Ala Arg Met Arg
150                 155                 160                 165

cct ggg act cgg ggg tta gat gta gcg gct gac ggc acc gtt caa ggg      643
Pro Gly Thr Arg Gly Leu Asp Val Ala Ala Asp Gly Thr Val Gln Gly
                170                 175                 180

caa cga cat ttg gct gca gtc gga cgg atg acg gaa gat gtg gtt ttg      691
Gln Arg His Leu Ala Ala Val Gly Arg Met Thr Glu Asp Val Val Leu
            185                 190                 195

ggt aat gac aca ttg tcg cga tca tta cat gac ata atc ccg aag tgg      739
Gly Asn Asp Thr Leu Ser Arg Ser Leu His Asp Ile Ile Pro Lys Trp
        200                 205                 210

gct cgt cga gtt atc cgc gac gcg agc acg tat ccc gat agg gta cat      787
Ala Arg Arg Val Ile Arg Asp Ala Ser Thr Tyr Pro Asp Arg Val His
    215                 220                 225

ggt act cca ccg ctt ccg gca cgg ttg gaa ccc tgg gcg gaa aag ctc      835
Gly Thr Pro Pro Leu Pro Ala Arg Leu Glu Pro Trp Ala Glu Lys Leu
230                 235                 240                 245

act tca gat ccg gcc aca tgc cgc cac ctg att gaa gaa ttc ggg agt      883
Thr Ser Asp Pro Ala Thr Cys Arg His Leu Ile Glu Glu Phe Gly Ser
                250                 255                 260

cct gtg aat gta ctc cat tca ggt tct atg cct cgt aat ata aat gag      931
Pro Val Asn Val Leu His Ser Gly Ser Met Pro Arg Asn Ile Asn Glu
            265                 270                 275
```

```
ttg gtt gac gcc ggc att cag atg ggg gtg gat act cga ata ttt ttt    979
Leu Val Asp Ala Gly Ile Gln Met Gly Val Asp Thr Arg Ile Phe Phe
        280                 285                 290

gcc cgc aaa gcg aat aag ggt ctt acc ttc gtt gat gcc gtt aaa gac   1027
Ala Arg Lys Ala Asn Lys Gly Leu Thr Phe Val Asp Ala Val Lys Asp
    295                 300                 305

acc ggt cat ggt gta gat gta gcc agt gaa cga gag tta tct cag gtg   1075
Thr Gly His Gly Val Asp Val Ala Ser Glu Arg Glu Leu Ser Gln Val
310                 315                 320                 325

ctt aat cgt gga gtc cca gga gag cgg atc att cta tcc gca gct atc   1123
Leu Asn Arg Gly Val Pro Gly Glu Arg Ile Ile Leu Ser Ala Ala Ile
                330                 335                 340

aaa ccg gac aga cta ttg gca tta gcg atc gaa aat ggc gtg atc atc   1171
Lys Pro Asp Arg Leu Leu Ala Leu Ala Ile Glu Asn Gly Val Ile Ile
            345                 350                 355

tct gtg gat tcg cgt gat gaa tta gat cgc att tcg gct ttg gtt ggt   1219
Ser Val Asp Ser Arg Asp Glu Leu Asp Arg Ile Ser Ala Leu Val Gly
        360                 365                 370

gac cgc gtt gca cga gtt gcg cct aga gta gct cca gat cct gca gtc   1267
Asp Arg Val Ala Arg Val Ala Pro Arg Val Ala Pro Asp Pro Ala Val
    375                 380                 385

tta cct cca act aga ttt ggt gag cgt gct gca gac tgg ggt aat cgg   1315
Leu Pro Pro Thr Arg Phe Gly Glu Arg Ala Ala Asp Trp Gly Asn Arg
390                 395                 400                 405

ctt acc gag gtg ata ccc ggc gtg gat att gtg ggt ctt cac gtt cac   1363
Leu Thr Glu Val Ile Pro Gly Val Asp Ile Val Gly Leu His Val His
                410                 415                 420

ctc cat ggc tat gct gca aaa gac cgt gct ctg gct ctg cag gaa tgt   1411
Leu His Gly Tyr Ala Ala Lys Asp Arg Ala Leu Ala Leu Gln Glu Cys
            425                 430                 435

tgc caa ctc gtc gat tct ctc aga gaa tgc ggg cat tcc cca cag ttt   1459
Cys Gln Leu Val Asp Ser Leu Arg Glu Cys Gly His Ser Pro Gln Phe
        440                 445                 450

att gac ctt gga gga ggg gtg cct atg agc tac att gaa tct gag gaa   1507
Ile Asp Leu Gly Gly Gly Val Pro Met Ser Tyr Ile Glu Ser Glu Glu
    455                 460                 465

gat tgg atc cgt tat caa tcc gct aaa tct gcg act tca gcc ggg tat   1555
Asp Trp Ile Arg Tyr Gln Ser Ala Lys Ser Ala Thr Ser Ala Gly Tyr
470                 475                 480                 485

gcc gaa tcc ttt acg tgg aaa gac gat ccg tta tct aat acg tac ccg   1603
Ala Glu Ser Phe Thr Trp Lys Asp Asp Pro Leu Ser Asn Thr Tyr Pro
                490                 495                 500

ttc tat cag acc cca gtg cgc ggt aat tgg ttg aaa gac gtg ctt tct   1651
Phe Tyr Gln Thr Pro Val Arg Gly Asn Trp Leu Lys Asp Val Leu Ser
            505                 510                 515
```

```
aag ggg gta gct cag atg ctc att gac cgg gga ttg cgg tta cac ata   1699
Lys Gly Val Ala Gln Met Leu Ile Asp Arg Gly Leu Arg Leu His Ile
        520                 525                 530

gag cct ggt cga agt tta cta gat ggg tgt ggc gtc act ctt gcc gaa   1747
Glu Pro Gly Arg Ser Leu Leu Asp Gly Cys Gly Val Thr Leu Ala Glu
    535                 540                 545

gtt gct ttt gtg aaa acc cga agt gac ggg ttg cct cta gtg gga ctg   1795
Val Ala Phe Val Lys Thr Arg Ser Asp Gly Leu Pro Leu Val Gly Leu
550                 555                 560                 565

gct atg aac cga acg cag tgc cgg act aca tcc gat gat ttt ctc att   1843
Ala Met Asn Arg Thr Gln Cys Arg Thr Thr Ser Asp Asp Phe Leu Ile
                570                 575                 580

gat ccc ctg cat atc act gac ggt gat gta ggc gag gaa atc gaa gca   1891
Asp Pro Leu His Ile Thr Asp Gly Asp Val Gly Glu Glu Ile Glu Ala
            585                 590                 595

tat cta gtg ggt gcc tac tgc atc gaa gat gag ctg att tta cgc cgg   1939
Tyr Leu Val Gly Ala Tyr Cys Ile Glu Asp Glu Leu Ile Leu Arg Arg
        600                 605                 610

cga atc cgc ttc ccg aga gga gtc aaa cca gga gat atc atc gga att   1987
Arg Ile Arg Phe Pro Arg Gly Val Lys Pro Gly Asp Ile Ile Gly Ile
    615                 620                 625

cct aac acc gca gga tac ttc atg cat atc ttg gaa agt gca tcg cac   2035
Pro Asn Thr Ala Gly Tyr Phe Met His Ile Leu Glu Ser Ala Ser His
630                 635                 640                 645

caa atc ccg ttg gcg aaa aat gta gtg tgg ccg gag ggg cag tta gac   2083
Gln Ile Pro Leu Ala Lys Asn Val Val Trp Pro Glu Gly Gln Leu Asp
                650                 655                 660

gat atc gat gcg gat taagacataa ccattcgcta atc                    2121
Asp Ile Asp Ala Asp
            665
```

<210> 46
<211> 666
<212> PRT
<213> Corynebacterium glutamicum

<400> 46

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Met Ile Pro Lys Pro Asp Val Thr Asp Leu Tyr Leu Glu Asp Leu Leu
  1               5                  10                  15

Asn Glu Gly Ser Glu Lys Ile Arg Ser Ala Lys Asp Leu Ser Glu Leu
             20                  25                  30

Arg Thr Val Leu Lys Glu Val Ser Ser Gln Ile Gln Glu Arg Ala Gly
         35                  40                  45

Lys Lys Asp Glu Glu Trp Gly Met Gly Ala Thr Trp Arg Glu Leu Tyr
     50                  55                  60

Pro Ser Ile Val Glu Arg Ala Ser Tyr Glu Gly Arg Asp Ser Leu Ile
 65                  70                  75                  80
```

```
Gly Phe Asp His Leu Ala Arg Glu Met Glu Arg Leu Ala Phe Gly Pro
                85                  90                  95

Pro Ser Glu Ser Phe Glu Tyr Leu Gln Glu Leu Val Lys Ser Gly Val
            100                 105                 110

Val Asp Ile Thr His Leu His Arg Gly Arg Glu Pro Leu Thr Asp Leu
        115                 120                 125

Val Arg Glu Leu Glu Ile Thr Val Val Ile Asp Ala Val Leu Pro Pro
    130                 135                 140

Pro Gly Val Val Pro Gly Thr Leu Val His Asn Leu Val Lys Glu Gly
145                 150                 155                 160

Tyr Ala Arg Met Arg Pro Gly Thr Arg Gly Leu Asp Val Ala Ala Asp
                165                 170                 175

Gly Thr Val Gln Gly Gln Arg His Leu Ala Ala Val Gly Arg Met Thr
            180                 185                 190

Glu Asp Val Val Leu Gly Asn Asp Thr Leu Ser Arg Ser Leu His Asp
        195                 200                 205

Ile Ile Pro Lys Trp Ala Arg Arg Val Ile Arg Asp Ala Ser Thr Tyr
    210                 215                 220

Pro Asp Arg Val His Gly Thr Pro Pro Leu Pro Ala Arg Leu Glu Pro
225                 230                 235                 240

Trp Ala Glu Lys Leu Thr Ser Asp Pro Ala Thr Cys Arg His Leu Ile
                245                 250                 255

Glu Glu Phe Gly Ser Pro Val Asn Val Leu His Ser Gly Ser Met Pro
            260                 265                 270

Arg Asn Ile Asn Glu Leu Val Asp Ala Gly Ile Gln Met Gly Val Asp
        275                 280                 285

Thr Arg Ile Phe Phe Ala Arg Lys Ala Asn Lys Gly Leu Thr Phe Val
    290                 295                 300

Asp Ala Val Lys Asp Thr Gly His Gly Val Asp Val Ala Ser Glu Arg
305                 310                 315                 320

Glu Leu Ser Gln Val Leu Asn Arg Gly Val Pro Gly Glu Arg Ile Ile
                325                 330                 335

Leu Ser Ala Ala Ile Lys Pro Asp Arg Leu Leu Ala Leu Ala Ile Glu
            340                 345                 350

Asn Gly Val Ile Ile Ser Val Asp Ser Arg Asp Glu Leu Asp Arg Ile
        355                 360                 365

Ser Ala Leu Val Gly Asp Arg Val Ala Arg Val Ala Pro Arg Val Ala
    370                 375                 380

Pro Asp Pro Ala Val Leu Pro Pro Thr Arg Phe Gly Glu Arg Ala Ala
385                 390                 395                 400
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Asp Trp Gly Asn Arg Leu Thr Glu Val Ile Pro Gly Val Asp Ile Val
405 410 415

Gly Leu His Val His Leu His Gly Tyr Ala Ala Lys Asp Arg Ala Leu
420 425 430

Ala Leu Gln Glu Cys Cys Gln Leu Val Asp Ser Leu Arg Glu Cys Gly
435 440 445

His Ser Pro Gln Phe Ile Asp Leu Gly Gly Gly Val Pro Met Ser Tyr
450 455 460

Ile Glu Ser Glu Glu Asp Trp Ile Arg Tyr Gln Ser Ala Lys Ser Ala
465 470 475 480

Thr Ser Ala Gly Tyr Ala Glu Ser Phe Thr Trp Lys Asp Asp Pro Leu
485 490 495

Ser Asn Thr Tyr Pro Phe Tyr Gln Thr Pro Val Arg Gly Asn Trp Leu
500 505 510

Lys Asp Val Leu Ser Lys Gly Val Ala Gln Met Leu Ile Asp Arg Gly
515 520 525

Leu Arg Leu His Ile Glu Pro Gly Arg Ser Leu Leu Asp Gly Cys Gly
530 535 540

Val Thr Leu Ala Glu Val Ala Phe Val Lys Thr Arg Ser Asp Gly Leu
545 550 555 560

Pro Leu Val Gly Leu Ala Met Asn Arg Thr Gln Cys Arg Thr Thr Ser
565 570 575

Asp Asp Phe Leu Ile Asp Pro Leu His Ile Thr Asp Gly Asp Val Gly
580 585 590

Glu Glu Ile Glu Ala Tyr Leu Val Gly Ala Tyr Cys Ile Glu Asp Glu
595 600 605

Leu Ile Leu Arg Arg Arg Ile Arg Phe Pro Arg Gly Val Lys Pro Gly
610 615 620

Asp Ile Ile Gly Ile Pro Asn Thr Ala Gly Tyr Phe Met His Ile Leu
625 630 635 640

Glu Ser Ala Ser His Gln Ile Pro Leu Ala Lys Asn Val Val Trp Pro
645 650 655

Glu Gly Gln Leu Asp Asp Ile Asp Ala Asp
660 665

<210> 47
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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<223> RXA01393

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agtaaaatga ttggttctta acatggttta atatagcttc atg aac ccc att caa 115
Met Asn Pro Ile Gln
1 5

ctg gac act ttg ctc tca atc att gat gaa ggc agc ttc gaa ggc gcc 163
Leu Asp Thr Leu Leu Ser Ile Ile Asp Glu Gly Ser Phe Glu Gly Ala
10 15 20

tcc tta gcc ctt tcc att tcc ccc tcg gcg gtg agt cag cgc gtt aaa 211
Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val Ser Gln Arg Val Lys
25 30 35

gct ctc gag cat cac gtg ggt cga gtg ttg gta tcg cgc acc caa ccg 259
Ala Leu Glu His His Val Gly Arg Val Leu Val Ser Arg Thr Gln Pro
40 45 50

gcc aaa gca acc gaa gcg ggt gaa gtc ctt gtg caa gca gcg cgg aaa 307
Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val Gln Ala Ala Arg Lys
55 60 65

atg gtg ttg ctg caa gca gaa act aaa gcg caa cta tct gga cgc ctt 355
Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln Leu Ser Gly Arg Leu
70 75 80 85

gct gaa atc ccg tta acc atc gcc atc aac gca gat tcg cta tcc aca 403
Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala Asp Ser Leu Ser Thr
90 95 100

tgg ttt cct ccc gtg ttc aac gag gta gct tct tgg ggt gga gca acg 451
Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser Trp Gly Gly Ala Thr
105 110 115

ctc acg ctg cgc ttg gaa gat gaa gcg cac aca tta tcc ttg ctg cgg 499
Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr Leu Ser Leu Leu Arg
120 125 130

cgt gga gat gtt tta gga gcg gta acc cgt gaa gct aat ccc gtg gcg 547
Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu Ala Asn Pro Val Ala
135 140 145

gga tgt gaa gta gta gaa ctt gga acc atg cgc cac ttg gcc att gca 595
Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg His Leu Ala Ile Ala
150 155 160 165

acc ccc tca ttg cgg gat gcc tac atg gtt gat ggg aaa cta gat tgg 643
Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp Gly Lys Leu Asp Trp
170 175 180

gct gcg atg ccc gtc tta cgc ttc ggt ccc aaa gat gtg ctt caa gac 691
Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys Asp Val Leu Gln Asp
185 190 195

cgt gac ctg gac ggg cgc gtc gat ggt cct gtg ggg cgc agg cgc gta 739
Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val Gly Arg Arg Arg Val
200 205 210

tcc att gtc ccg tcg gcg gaa ggt ttt ggt gag gca att cgc cga ggc 787

Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu Ala Ile Arg Arg Gly
215 220 225

ctt ggt tgg gga ctt ctt ccc gaa acc caa gct gct ccc atg cta aaa 835
Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala Ala Pro Met Leu Lys
230 235 240 245

gca gga gaa gtg atc ctc ctc gat gag ata ccc att gac aca ccg atg 883
Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro Ile Asp Thr Pro Met
250 255 260

tat tgg caa cga tgg cgc ctg gaa tct aga tct cta gct aga ctc aca 931
Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser Leu Ala Arg Leu Thr
265 270 275

gac gcc gtc gtt gat gca gca atc gag gga ttg cgg cct tagttacttc 980
Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu Arg Pro
280 285 290

tgaaaaggtt cag 993

<210> 48
<211> 290
<212> PRT
<213> Corynebacterium glutamicum

<400> 48
Met Asn Pro Ile Gln Leu Asp Thr Leu Leu Ser Ile Ile Asp Glu Gly
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Ser Phe Glu Gly Ala Ser Leu Ala Leu Ser Ile Ser Pro Ser Ala Val
20 25 30

Ser Gln Arg Val Lys Ala Leu Glu His His Val Gly Arg Val Leu Val
35 40 45

Ser Arg Thr Gln Pro Ala Lys Ala Thr Glu Ala Gly Glu Val Leu Val
50 55 60

Gln Ala Ala Arg Lys Met Val Leu Leu Gln Ala Glu Thr Lys Ala Gln
65 70 75 80

Leu Ser Gly Arg Leu Ala Glu Ile Pro Leu Thr Ile Ala Ile Asn Ala
85 90 95

Asp Ser Leu Ser Thr Trp Phe Pro Pro Val Phe Asn Glu Val Ala Ser
100 105 110

Trp Gly Gly Ala Thr Leu Thr Leu Arg Leu Glu Asp Glu Ala His Thr
115 120 125

Leu Ser Leu Leu Arg Arg Gly Asp Val Leu Gly Ala Val Thr Arg Glu
130 135 140

Ala Asn Pro Val Ala Gly Cys Glu Val Val Glu Leu Gly Thr Met Arg
145 150 155 160

His Leu Ala Ile Ala Thr Pro Ser Leu Arg Asp Ala Tyr Met Val Asp
165 170 175

```
Gly Lys Leu Asp Trp Ala Ala Met Pro Val Leu Arg Phe Gly Pro Lys
            180                 185                 190

Asp Val Leu Gln Asp Arg Asp Leu Asp Gly Arg Val Asp Gly Pro Val
        195                 200                 205

Gly Arg Arg Arg Val Ser Ile Val Pro Ser Ala Glu Gly Phe Gly Glu
    210                 215                 220

Ala Ile Arg Arg Gly Leu Gly Trp Gly Leu Leu Pro Glu Thr Gln Ala
225                 230                 235                     240

Ala Pro Met Leu Lys Ala Gly Glu Val Ile Leu Leu Asp Glu Ile Pro
                245                 250                 255

Ile Asp Thr Pro Met Tyr Trp Gln Arg Trp Arg Leu Glu Ser Arg Ser
            260                 265                 270

Leu Ala Arg Leu Thr Asp Ala Val Val Asp Ala Ala Ile Glu Gly Leu
        275                 280                 285

Arg Pro
    290


<210> 49
<211> 1626
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1603)
<223> RXA00241

<400> 49
ggtctccagc ctttctaaac aattcatctg cacttgatta attggcccca agattacgcg 60

aagtttagcg acttcgccgt acgtcaacta cgttaaatga gtg aat act caa tca    115
                                         Val Asn Thr Gln Ser
                                          1               5

gat tct gcg ggg tct caa ggt gca gcg gcc aca agt cgt act gta tct    163
Asp Ser Ala Gly Ser Gln Gly Ala Ala Ala Thr Ser Arg Thr Val Ser
                10                  15                  20

att aga acc ctc atc gcg ctg atc atc gga tcg acc gtc ggc gcg gga    211
Ile Arg Thr Leu Ile Ala Leu Ile Ile Gly Ser Thr Val Gly Ala Gly
            25                  30                  35

att ttc tcc atc cct caa aac atc ggc tca gtc gca ggt ccc ggc gcg    259
Ile Phe Ser Ile Pro Gln Asn Ile Gly Ser Val Ala Gly Pro Gly Ala
        40                  45                  50

atg ctc atc ggc tgg ctg atc gcc ggt gtg ggc atg ttg tcc gta gcg    307
Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly Met Leu Ser Val Ala
    55                  60                  65

ttc gtg ttc cat gtt ctt gcc cgc cgt aaa cct cac ctc gat tct ggc    355
Phe Val Phe His Val Leu Ala Arg Arg Lys Pro His Leu Asp Ser Gly
 70                  75                  80                  85
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```
gtc tac gca tat gcg cgt gtt gga ttg ggc gat tat gta ggt ttc tcc     403
Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp Tyr Val Gly Phe Ser
                 90                  95                 100

tcc gct tgg ggt tat tgg ctg ggt tca gtc atc gcc caa gtt ggc tac     451
Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile Ala Gln Val Gly Tyr
            105                 110                 115

gca acg tta ttt ttc tcc acg ttg ggc cac tac gta ccg ctg ttt tcc     499
Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr Val Pro Leu Phe Ser
        120                 125                 130

caa gat cat cca ttt gtg tca gcg ttg gca gtt agc gct ttg acc tgg     547
Gln Asp His Pro Phe Val Ser Ala Leu Ala Val Ser Ala Leu Thr Trp
    135                 140                 145

ctg gtg ttt gga gtt gtt tcc cga gga att agc caa gct gct ttc ttg     595
Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser Gln Ala Ala Phe Leu
150                 155                 160                 165

aca acg gtc acc acc gtg gcc aaa att ctg cct ctg ttg tgc ttc atc     643
Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro Leu Leu Cys Phe Ile
                170                 175                 180

atc ctt gtt gca ttc ttg ggc ttt agc tgg gag aag ttc act gtt gat     691
Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu Lys Phe Thr Val Asp
            185                 190                 195

tta tgg gcg cgt gat ggt ggc gtg ggc agc att ttt gat cag gtg cgc     739
Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile Phe Asp Gln Val Arg
        200                 205                 210

ggc atc atg gtg tac acc gtg tgg gtg ttc atc ggt atc gaa ggt gca     787
Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile Gly Ile Glu Gly Ala
    215                 220                 225

tcg gta tat tcc cgc cag gca cgc tca cgc agt gat gtc agc cga gct     835
Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser Asp Val Ser Arg Ala
230                 235                 240                 245

acc gtg att ggt ttt gtg gct gtt ctc ctt ttg ctg gtg tcg att tct     883
Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu Leu Val Ser Ile Ser
                250                 255                 260

tcg ctg agc ttc ggt gta ctg acc caa caa gag ctc gct gcg tta cca     931
Ser Leu Ser Phe Gly Val Leu Thr Gln Gln Glu Leu Ala Ala Leu Pro
            265                 270                 275

gat aat tcc atg gcg tcg gtg ctc gaa gct gtt gtt ggt cca tgg ggt     979
Asp Asn Ser Met Ala Ser Val Leu Glu Ala Val Val Gly Pro Trp Gly
        280                 285                 290

gcc gca ttg att tcg ttg ggt ctg tgt ctt tcg gtt ctt ggg gcc tat     1027
Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser Val Leu Gly Ala Tyr
    295                 300                 305

gtg tcc tgg cag atg ctc tgc gca gaa cca ctg gcg ttg atg gca atg     1075
Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu Ala Leu Met Ala Met
310                 315                 320                 325
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gat ggc ctc att cca agc aaa atc ggg gcc atc aac agc cgc ggt gct      1123
Asp Gly Leu Ile Pro Ser Lys Ile Gly Ala Ile Asn Ser Arg Gly Ala
                330                 335                 340

gcc tgg atg gct cag ctg atc tcc acc atc gtg att cag att ttc atc      1171
Ala Trp Met Ala Gln Leu Ile Ser Thr Ile Val Ile Gln Ile Phe Ile
            345                 350                 355

atc att ttc ttc ctc aac gag acc acc tac gtc tcc atg gtg caa ttg      1219
Ile Ile Phe Phe Leu Asn Glu Thr Thr Tyr Val Ser Met Val Gln Leu
        360                 365                 370

gct acc aac cta tac ttg gtg cct tac ctg ttc tct gcc ttt tat ctg      1267
Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe Ser Ala Phe Tyr Leu
    375                 380                 385

gtc atg ctg gca aca cgt gga aaa gga atc acc cac cca cat gcc ggc      1315
Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr His Pro His Ala Gly
390                 395                 400                 405

aca cgt ttt gat gat tcc ggt cca gag ata tcc cgc cga gaa aac cgc      1363
Thr Arg Phe Asp Asp Ser Gly Pro Glu Ile Ser Arg Arg Glu Asn Arg
                410                 415                 420

aaa cac ctc atc gtc ggt tta gta gca acg gtg tat tca gtg tgg ctg      1411
Lys His Leu Ile Val Gly Leu Val Ala Thr Val Tyr Ser Val Trp Leu
            425                 430                 435

ttt tac gct gca gaa ccg cag ttt gtc ctc ttc gga gcc atg gcg atg      1459
Phe Tyr Ala Ala Glu Pro Gln Phe Val Leu Phe Gly Ala Met Ala Met
        440                 445                 450

ctt ccc ggc tta atc ccc tat gtg tgg aca agg att tat cgt ggc gaa      1507
Leu Pro Gly Leu Ile Pro Tyr Val Trp Thr Arg Ile Tyr Arg Gly Glu
    455                 460                 465

cag gtg ttt aac cgc ttt gaa atc ggc gtg gtt gtt gtc ctg gtc gtt      1555
Gln Val Phe Asn Arg Phe Glu Ile Gly Val Val Val Val Leu Val Val
470                 475                 480                 485

gct gcc agc gcg ggc gtt att ggt ttg gtc aac gga tca cta tcg ctt      1603
Ala Ala Ser Ala Gly Val Ile Gly Leu Val Asn Gly Ser Leu Ser Leu
                490                 495                 500

taaacaccga aaccttcctg cta                                           1626
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<210> 50
<211> 501
<212> PRT
<213> Corynebacterium glutamicum

<400> 50

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Val Asn Thr Gln Ser Asp Ser Ala Gly Ser Gln Gly Ala Ala Ala Thr
  1               5                  10                  15

Ser Arg Thr Val Ser Ile Arg Thr Leu Ile Ala Leu Ile Ile Gly Ser
            20                  25                  30

Thr Val Gly Ala Gly Ile Phe Ser Ile Pro Gln Asn Ile Gly Ser Val
        35                  40                  45
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```
Ala Gly Pro Gly Ala Met Leu Ile Gly Trp Leu Ile Ala Gly Val Gly
     50                  55                  60

Met Leu Ser Val Ala Phe Val Phe His Val Leu Ala Arg Arg Lys Pro
65                  70                  75                  80

His Leu Asp Ser Gly Val Tyr Ala Tyr Ala Arg Val Gly Leu Gly Asp
                85                  90                  95

Tyr Val Gly Phe Ser Ser Ala Trp Gly Tyr Trp Leu Gly Ser Val Ile
            100                 105                 110

Ala Gln Val Gly Tyr Ala Thr Leu Phe Phe Ser Thr Leu Gly His Tyr
        115                 120                 125

Val Pro Leu Phe Ser Gln Asp His Pro Phe Val Ser Ala Leu Ala Val
    130                 135                 140

Ser Ala Leu Thr Trp Leu Val Phe Gly Val Val Ser Arg Gly Ile Ser
145                 150                 155                 160

Gln Ala Ala Phe Leu Thr Thr Val Thr Thr Val Ala Lys Ile Leu Pro
                165                 170                 175

Leu Leu Cys Phe Ile Ile Leu Val Ala Phe Leu Gly Phe Ser Trp Glu
            180                 185                 190

Lys Phe Thr Val Asp Leu Trp Ala Arg Asp Gly Gly Val Gly Ser Ile
        195                 200                 205

Phe Asp Gln Val Arg Gly Ile Met Val Tyr Thr Val Trp Val Phe Ile
    210                 215                 220

Gly Ile Glu Gly Ala Ser Val Tyr Ser Arg Gln Ala Arg Ser Arg Ser
225                 230                 235                 240

Asp Val Ser Arg Ala Thr Val Ile Gly Phe Val Ala Val Leu Leu Leu
                245                 250                 255

Leu Val Ser Ile Ser Ser Leu Ser Phe Gly Val Leu Thr Gln Gln Glu
            260                 265                 270

Leu Ala Ala Leu Pro Asp Asn Ser Met Ala Ser Val Leu Glu Ala Val
        275                 280                 285

Val Gly Pro Trp Gly Ala Ala Leu Ile Ser Leu Gly Leu Cys Leu Ser
    290                 295                 300

Val Leu Gly Ala Tyr Val Ser Trp Gln Met Leu Cys Ala Glu Pro Leu
305                 310                 315                 320

Ala Leu Met Ala Met Asp Gly Leu Ile Pro Ser Lys Ile Gly Ala Ile
                325                 330                 335

Asn Ser Arg Gly Ala Ala Trp Met Ala Gln Leu Ile Ser Thr Ile Val
            340                 345                 350

Ile Gln Ile Phe Ile Ile Ile Phe Phe Leu Asn Glu Thr Thr Tyr Val
        355                 360                 365
```

```
Ser Met Val Gln Leu Ala Thr Asn Leu Tyr Leu Val Pro Tyr Leu Phe
    370                 375                 380

Ser Ala Phe Tyr Leu Val Met Leu Ala Thr Arg Gly Lys Gly Ile Thr
385                 390                 395                 400

His Pro His Ala Gly Thr Arg Phe Asp Asp Ser Gly Pro Glu Ile Ser
                405                 410                 415

Arg Arg Glu Asn Arg Lys His Leu Ile Val Gly Leu Val Ala Thr Val
            420                 425                 430

Tyr Ser Val Trp Leu Phe Tyr Ala Ala Glu Pro Gln Phe Val Leu Phe
        435                 440                 445

Gly Ala Met Ala Met Leu Pro Gly Leu Ile Pro Tyr Val Trp Thr Arg
    450                 455                 460

Ile Tyr Arg Gly Glu Gln Val Phe Asn Arg Phe Glu Ile Gly Val Val
465                 470                 475                 480

Val Val Leu Val Val Ala Ala Ser Ala Gly Val Ile Gly Leu Val Asn
                485                 490                 495

Gly Ser Leu Ser Leu
            500
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<210> 51
<211> 822
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(799)
<223> RXA01394

<400> 51

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tcattttact taagtacttc cataggtcac gatggtgatc atg gaa atc ttc att   115
                                            Met Glu Ile Phe Ile
                                              1               5

aca ggt ctg ctt ttg ggg gcc agt ctt tta ctg tcc atc gga ccg cag   163
Thr Gly Leu Leu Leu Gly Ala Ser Leu Leu Leu Ser Ile Gly Pro Gln
                  10                  15                  20

aat gta ctg gtg att aaa caa gga att aag cgc gaa gga ctc att gcg   211
Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg Glu Gly Leu Ile Ala
              25                  30                  35

gtt ctt ctc gtg tgt tta att tct gac gtc ttt ttg ttc atc gcc ggc   259
Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe Leu Phe Ile Ala Gly
          40                  45                  50

acc ttg ggc gtt gat ctt ttg tcc aat gcc gcg ccg atc gtg ctc gat   307
Thr Leu Gly Val Asp Leu Leu Ser Asn Ala Ala Pro Ile Val Leu Asp
      55                  60                  65
```

```
att atg cgc tgg ggt ggc atc gct tac ctg tta tgg ttt gcc gtc atg   355
Ile Met Arg Trp Gly Gly Ile Ala Tyr Leu Leu Trp Phe Ala Val Met
 70                  75                  80                  85

gca gcg aaa gac gcc atg aca aac aag gtg gaa gcg cca cag atc att   403
Ala Ala Lys Asp Ala Met Thr Asn Lys Val Glu Ala Pro Gln Ile Ile
                 90                  95                 100

gaa gaa aca gaa cca acc gtg ccc gat gac acg cct ttg ggc ggt tcg   451
Glu Glu Thr Glu Pro Thr Val Pro Asp Asp Thr Pro Leu Gly Gly Ser
            105                 110                 115

gcg gtg gcc act gac acg cgc aac cgg gtg cgg gtg gag gtg agc gtc   499
Ala Val Ala Thr Asp Thr Arg Asn Arg Val Arg Val Glu Val Ser Val
        120                 125                 130

gat aag cag cgg gtt tgg gta aag ccc atg ttg atg gca atc gtg ctg   547
Asp Lys Gln Arg Val Trp Val Lys Pro Met Leu Met Ala Ile Val Leu
    135                 140                 145

acc tgg ttg aac ccg aat gcg tat ttg gac gcg ttt gtg ttt atc ggc   595
Thr Trp Leu Asn Pro Asn Ala Tyr Leu Asp Ala Phe Val Phe Ile Gly
150                 155                 160                 165

ggc gtc ggc gcg caa tac ggc gac acc gga cgg tgg att ttc gcc gct   643
Gly Val Gly Ala Gln Tyr Gly Asp Thr Gly Arg Trp Ile Phe Ala Ala
                170                 175                 180

ggc gcg ttc gcg gca agc ctg atc tgg ttc ccg ctg gtg ggt ttc ggc   691
Gly Ala Phe Ala Ala Ser Leu Ile Trp Phe Pro Leu Val Gly Phe Gly
            185                 190                 195

gca gca gca ttg tca cgc ccg ctg tcc agc ccc aag gtg tgg cgc tgg   739
Ala Ala Ala Leu Ser Arg Pro Leu Ser Ser Pro Lys Val Trp Arg Trp
        200                 205                 210

atc aac gtc gtc gtg gca gtt gtg atg acc gca ttg gcc atc aaa ctg   787
Ile Asn Val Val Val Ala Val Val Met Thr Ala Leu Ala Ile Lys Leu
    215                 220                 225

atg ttg atg ggt tagttttcgc gggttttgga atc                        822
Met Leu Met Gly
230
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<210> 52
<211> 233
<212> PRT
<213> Corynebacterium glutamicum

<400> 52

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Met Glu Ile Phe Ile Thr Gly Leu Leu Leu Gly Ala Ser Leu Leu Leu
  1               5                  10                  15

Ser Ile Gly Pro Gln Asn Val Leu Val Ile Lys Gln Gly Ile Lys Arg
             20                  25                  30

Glu Gly Leu Ile Ala Val Leu Leu Val Cys Leu Ile Ser Asp Val Phe
         35                  40                  45

Leu Phe Ile Ala Gly Thr Leu Gly Val Asp Leu Leu Ser Asn Ala Ala
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50 55 60

Pro Ile Val Leu Asp Ile Met Arg Trp Gly Gly Ile Ala Tyr Leu Leu
65 70 75 80

Trp Phe Ala Val Met Ala Ala Lys Asp Ala Met Thr Asn Lys Val Glu
85 90 95

Ala Pro Gln Ile Ile Glu Glu Thr Glu Pro Thr Val Pro Asp Asp Thr
100 105 110

Pro Leu Gly Gly Ser Ala Val Ala Thr Asp Thr Arg Asn Arg Val Arg
115 120 125

Val Glu Val Ser Val Asp Lys Gln Arg Val Trp Val Lys Pro Met Leu
130 135 140

Met Ala Ile Val Leu Thr Trp Leu Asn Pro Asn Ala Tyr Leu Asp Ala
145 150 155 160

Phe Val Phe Ile Gly Gly Val Gly Ala Gln Tyr Gly Asp Thr Gly Arg
165 170 175

Trp Ile Phe Ala Ala Gly Ala Phe Ala Ala Ser Leu Ile Trp Phe Pro
180 185 190

Leu Val Gly Phe Gly Ala Ala Ala Leu Ser Arg Pro Leu Ser Ser Pro
195 200 205

Lys Val Trp Arg Trp Ile Asn Val Val Val Ala Val Val Met Thr Ala
210 215 220

Leu Ala Ile Lys Leu Met Leu Met Gly
225 230

<210> 53
<211> 1026
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1003)
<223> RXA00865

<400> 53
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tttaaccccc aaatgaggga agaaggtaac cttgaactct atg agc aca ggt tta 115
Met Ser Thr Gly Leu
1 5

aca gct aag acc gga gta gag cac ttc ggc acc gtt gga gta gca atg 163
Thr Ala Lys Thr Gly Val Glu His Phe Gly Thr Val Gly Val Ala Met
10 15 20

gtt act cca ttc acg gaa tcc gga gac atc gat atc gct gct ggc cgc 211
Val Thr Pro Phe Thr Glu Ser Gly Asp Ile Asp Ile Ala Ala Gly Arg
25 30 35

```
gaa gtc gcg gct tat ttg gtt gat aag ggc ttg gat tct ttg gtt ctc     259
Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu Asp Ser Leu Val Leu
        40                  45                  50

gcg ggc acc act ggt gaa tcc cca acg aca acc gcc gct gaa aaa cta     307
Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr Ala Ala Glu Lys Leu
    55                  60                  65

gaa ctg ctc aag gcc gtt cgt gag gaa gtt ggg gat cgg gcg aag ctc     355
Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly Asp Arg Ala Lys Leu
70                  75                  80                  85

atc gcc ggt gtc gga acc aac aac acg cgg aca tct gtg gaa ctt gcg     403
Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr Ser Val Glu Leu Ala
                90                  95                  100

gaa gct gct gct tct gct ggc gca gac ggc ctt tta gtt gta act cct     451
Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu Leu Val Val Thr Pro
            105                 110                 115

tat tac tcc aag ccg agc caa gag gga ttg ctg gcg cac ttc ggt gca     499
Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu Ala His Phe Gly Ala
        120                 125                 130

att gct gca gca aca gag gtt cca att tgt ctc tat gac att cct ggt     547
Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu Tyr Asp Ile Pro Gly
    135                 140                 145

cgg tca ggt att cca att gag tct gat acc atg aga cgc ctg agt gaa     595
Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met Arg Arg Leu Ser Glu
150                 155                 160                 165

tta cct acg att ttg gcg gtc aag gac gcc aag ggt gac ctc gtt gca     643
Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys Gly Asp Leu Val Ala
                170                 175                 180

gcc acg tca ttg atc aaa gaa acg gga ctt gcc tgg tat tca ggc gat     691
Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala Trp Tyr Ser Gly Asp
            185                 190                 195

gac cca cta aac ctt gtt tgg ctt gct ttg ggc gga tca ggt ttc att     739
Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly Gly Ser Gly Phe Ile
        200                 205                 210

tcc gta att gga cat gca gcc ccc aca gca tta cgt gag ttg tac aca     787
Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu Arg Glu Leu Tyr Thr
    215                 220                 225

agc ttc gag gaa ggc gac ctc gtc cgt gcg cgg gaa atc aac gcc aaa     835
Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg Glu Ile Asn Ala Lys
230                 235                 240                 245

cta tca ccg ctg gta gct gcc caa ggt cgc ttg ggt gga gtc agc ttg     883
Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu Gly Gly Val Ser Leu
                250                 255                 260

gca aaa gct gct ctg cgt ctg cag ggc atc aac gta gga gat cct cga     931
Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn Val Gly Asp Pro Arg
            265                 270                 275

ctt cca att atg gct cca aat gag cag gaa ctt gag gct ctc cga gaa     979
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Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu Glu Ala Leu Arg Glu
280 285 290

gac atg aaa aaa gct gga gtt cta taaatatgaa tgattcccga aat 1026
Asp Met Lys Lys Ala Gly Val Leu
295 300

<210> 54
<211> 301
<212> PRT
<213> Corynebacterium glutamicum

<400> 54
Met Ser Thr Gly Leu Thr Ala Lys Thr Gly Val Glu His Phe Gly Thr
1 5 10 15

Val Gly Val Ala Met Val Thr Pro Phe Thr Glu Ser Gly Asp Ile Asp
20 25 30

Ile Ala Ala Gly Arg Glu Val Ala Ala Tyr Leu Val Asp Lys Gly Leu
35 40 45

Asp Ser Leu Val Leu Ala Gly Thr Thr Gly Glu Ser Pro Thr Thr Thr
50 55 60

Ala Ala Glu Lys Leu Glu Leu Leu Lys Ala Val Arg Glu Glu Val Gly
65 70 75 80

Asp Arg Ala Lys Leu Ile Ala Gly Val Gly Thr Asn Asn Thr Arg Thr
85 90 95

Ser Val Glu Leu Ala Glu Ala Ala Ala Ser Ala Gly Ala Asp Gly Leu
100 105 110

Leu Val Val Thr Pro Tyr Tyr Ser Lys Pro Ser Gln Glu Gly Leu Leu
115 120 125

Ala His Phe Gly Ala Ile Ala Ala Ala Thr Glu Val Pro Ile Cys Leu
130 135 140

Tyr Asp Ile Pro Gly Arg Ser Gly Ile Pro Ile Glu Ser Asp Thr Met
145 150 155 160

Arg Arg Leu Ser Glu Leu Pro Thr Ile Leu Ala Val Lys Asp Ala Lys
165 170 175

Gly Asp Leu Val Ala Ala Thr Ser Leu Ile Lys Glu Thr Gly Leu Ala
180 185 190

Trp Tyr Ser Gly Asp Asp Pro Leu Asn Leu Val Trp Leu Ala Leu Gly
195 200 205

Gly Ser Gly Phe Ile Ser Val Ile Gly His Ala Ala Pro Thr Ala Leu
210 215 220

Arg Glu Leu Tyr Thr Ser Phe Glu Glu Gly Asp Leu Val Arg Ala Arg
225 230 235 240

Glu Ile Asn Ala Lys Leu Ser Pro Leu Val Ala Ala Gln Gly Arg Leu
245 250 255

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Gly Gly Val Ser Leu Ala Lys Ala Ala Leu Arg Leu Gln Gly Ile Asn
            260                 265                 270

Val Gly Asp Pro Arg Leu Pro Ile Met Ala Pro Asn Glu Gln Glu Leu
        275                 280                 285

Glu Ala Leu Arg Glu Asp Met Lys Lys Ala Gly Val Leu
    290                 295                 300


<210> 55
<211> 1071
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1048)
<223> RXS02021

<400> 55
ttgggtcgcc gaggagatct aatcctggtt tgagttcaga gttcacaggt ttaagcctac 60

aaaccttagt taaaacatga tggaagcggt cgattaaaaa atg agt gaa aac att   115
                                              Met Ser Glu Asn Ile
                                                1               5

cgc gga gcc caa gca gtt gga atc gca aat atc gcc atg gac ggg acc   163
Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile Ala Met Asp Gly Thr
                10                  15                  20

atc ctg gac acg tgg tac cca gaa ccc caa att ttc aac ccg gat cag   211
Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile Phe Asn Pro Asp Gln
            25                  30                  35

tgg gct gaa cgc tac cca ttg gaa gtg ggc acc aca cgc ctc gga gca   259
Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr Thr Arg Leu Gly Ala
        40                  45                  50

aac gaa ctc acc cca cgg atg ctg cag ttg gta aaa ctg gac caa gat   307
Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val Lys Leu Asp Gln Asp
    55                  60                  65

cgc ctc gtc gaa cag gta gca gtc cgc acc gtt atc ccc gat ctg tct   355
Arg Leu Val Glu Gln Val Ala Val Arg Thr Val Ile Pro Asp Leu Ser
70                  75                  80                  85

caa cct cca gta gac gcg cac gat gtt tac ctg cgc ctc cac ctg ctt   403
Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu Arg Leu His Leu Leu
                90                  95                  100

tcc cac cgg ctg gtc cgc ccc cac gaa atg cac atg caa aac acc ttg   451
Ser His Arg Leu Val Arg Pro His Glu Met His Met Gln Asn Thr Leu
            105                 110                 115

gag ctg ctg tcc gac gtg gtg tgg aca aac aag ggc cct tgc ctt cct   499
Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys Gly Pro Cys Leu Pro
        120                 125                 130

gaa aac ttt gag tgg gtg cgt ggt gct ctg cgg tcc cgc gga ctc atc   547
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Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg Ser Arg Gly Leu Ile
    135   140   145

cac gtc tac tgt gtg gac cgt ctt ccc cgc atg gtc gac tat gtg gtt   595
His Val Tyr Cys Val Asp Arg Leu Pro Arg Met Val Asp Tyr Val Val
150   155   160   165

ccc cct gga gtc cgc atc tcc gaa gca gaa cgc gtg cgc cta ggt gca   643
Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg Val Arg Leu Gly Ala
                170   175   180

tac ctt gct ccg ggt acc tct gtg ctg cgt gaa ggt ttc gtg tct ttc   691
Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu Gly Phe Val Ser Phe
            185   190   195

aac tcc ggc acc ttg ggt gcc gca aag gtg gaa ggc cgc ctg agt tcc   739
Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu Gly Arg Leu Ser Ser
        200   205   210

ggt gtg gtc atc ggt gaa ggt tcc gag att gga ctg tct tct act att   787
Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly Leu Ser Ser Thr Ile
    215   220   225

cag tcc ccg aga gat gaa cag cgc cgc cgt ttg ccg ttg agc atc ggc   835
Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu Pro Leu Ser Ile Gly
230   235   240   245

caa aac tgc aac ttt ggt gtc agc tcc gga atc atc gga gtc agt ctg   883
Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile Ile Gly Val Ser Leu
                250   255   260

gga gac aat tgc gac atc gga aat aac att gtc ttg gat gga gat acc   931
Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val Leu Asp Gly Asp Thr
            265   270   275

ccc att tgg ttc gca gcc gat gag gag tta cgc act atc gac tcc atc   979
Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg Thr Ile Asp Ser Ile
        280   285   290

gaa ggc caa gca aat tgg tca atc aag cgt gaa tcc ggc ttc cat gag   1027
Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu Ser Gly Phe His Glu
    295   300   305

cca gtt gcc cgc ctc aaa gct tgacccattt tcataaccag tgc   1071
Pro Val Ala Arg Leu Lys Ala
310   315

<210> 56
<211> 316
<212> PRT
<213> Corynebacterium glutamicum

<400> 56
Met Ser Glu Asn Ile Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile
  1   5   10   15

Ala Met Asp Gly Thr Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile
            20   25   30

Phe Asn Pro Asp Gln Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr

```
        35                  40                  45

Thr Arg Leu Gly Ala Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val
    50                  55                  60

Lys Leu Asp Gln Asp Arg Leu Val Glu Gln Val Ala Val Arg Thr Val
65                  70                  75                  80

Ile Pro Asp Leu Ser Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu
                85                  90                  95

Arg Leu His Leu Leu Ser His Arg Leu Val Arg Pro His Glu Met His
            100                 105                 110

Met Gln Asn Thr Leu Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys
        115                 120                 125

Gly Pro Cys Leu Pro Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg
    130                 135                 140

Ser Arg Gly Leu Ile His Val Tyr Cys Val Asp Arg Leu Pro Arg Met
145                 150                 155                 160

Val Asp Tyr Val Val Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg
                165                 170                 175

Val Arg Leu Gly Ala Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu
            180                 185                 190

Gly Phe Val Ser Phe Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu
        195                 200                 205

Gly Arg Leu Ser Ser Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly
    210                 215                 220

Leu Ser Ser Thr Ile Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu
225                 230                 235                 240

Pro Leu Ser Ile Gly Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile
                245                 250                 255

Ile Gly Val Ser Leu Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val
            260                 265                 270

Leu Asp Gly Asp Thr Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg
        275                 280                 285

Thr Ile Asp Ser Ile Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu
    290                 295                 300

Ser Gly Phe His Glu Pro Val Ala Arg Leu Lys Ala
305                 310                 315
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<210> 57
<211> 1296
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(1273)
<223> RXS02157

<400> 57
gggtggaatt ggcacgatgg tgctgccgga tgtttttgat cgggagaatt atcctgaagg 60

caccgttttt agaaaagacg acaaggatgg ggaactgtaa atg agc acg ctg gaa 115
Met Ser Thr Leu Glu
1 5

act tgg cca cag gtc att att aat acg tac ggc acc cca cca gtt gag 163
Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly Thr Pro Pro Val Glu
10 15 20

ctg gtg tcc ggc aag ggc gca acc gtc act gat gac cag ggc aat gtc 211
Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp Asp Gln Gly Asn Val
25 30 35

tac atc gac ttg ctc gcg ggc atc gca gtc aac gcg ttg ggc cac gcc 259
Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn Ala Leu Gly His Ala
40 45 50

cac ccg gcg atc atc gag gcg gtc acc aac cag atc ggc caa ctt ggt 307
His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln Ile Gly Gln Leu Gly
55 60 65

cac gtc tca aac ttg ttc gca tcc agg ccc gtc gtc gag gtc gcc gag 355
His Val Ser Asn Leu Phe Ala Ser Arg Pro Val Val Glu Val Ala Glu
70 75 80 85

gag ctc atc aag cgt ttt tcg ctt gac gac gcc acc ctc gcc gcg caa 403
Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala Thr Leu Ala Ala Gln
90 95 100

acc cgg gtt ttc ttc tgc aac tcg ggc gcc gaa gca aac gag gct gct 451
Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu Ala Asn Glu Ala Ala
105 110 115

ttc aag att gca cgc ttg act ggt cgt tcc cgg att ctg gct gca gtt 499
Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg Ile Leu Ala Ala Val
120 125 130

cat ggt ttc cac ggc cgc acc atg ggt tcc ctc gcg ctg act ggc cag 547
His Gly Phe His Gly Arg Thr Met Gly Ser Leu Ala Leu Thr Gly Gln
135 140 145

cca gac aag cgt gaa gcg ttc ctg cca atg cca agc ggt gtg gag ttc 595
Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro Ser Gly Val Glu Phe
150 155 160 165

tac cct tac ggc gac acc gat tac ttg cgc aaa atg gta gaa acc aac 643
Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys Met Val Glu Thr Asn
170 175 180

cca acg gat gtg gct gct atc ttc ctc gag cca atc cag ggt gaa acg 691
Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro Ile Gln Gly Glu Thr
185 190 195

ggc gtt gtt cca gca cct gaa gga ttc ctc aag gca gtg cgc gag ctg 739
Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys Ala Val Arg Glu Leu
200 205 210

tgc gat gag tac ggc atc ttg atg atc acc gat gaa gtc cag act ggc 787
Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp Glu Val Gln Thr Gly
215 220 225

gtt ggc cgt acc ggc gat ttc ttt gca cat cag cac gat ggc gtt gtt 835
Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln His Asp Gly Val Val
230 235 240 245

ccc gat gtg gtg acc atg gcc aag gga ctt ggc ggc ggt ctt ccc atc 883
Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly Gly Gly Leu Pro Ile
250 255 260

ggt gct tgt ttg gcc act ggc cgt gca gct gaa ttg atg acc cca ggc 931
Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu Leu Met Thr Pro Gly
265 270 275

aag cac ggc acc act ttc ggt ggc aac cca gtt gct tgt gca gct gcc 979
Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val Ala Cys Ala Ala Ala
280 285 290

aag gca gtg ctg tct gtt gtc gat gac gct ttc tgc gca gaa gtt gcc 1027
Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe Cys Ala Glu Val Ala
295 300 305

cgc aag ggc gag ctg ttc aag gaa ctt ctt gcc aag gtt gac ggc gtt 1075
Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala Lys Val Asp Gly Val
310 315 320 325

gta gac gtc cgt ggc agg ggc ttg atg ttg ggc gtg gtg ctg gag cgc 1123
Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly Val Val Leu Glu Arg
330 335 340

gac gtc gca aag caa gct gtt ctt gat ggt ttt aag cac ggc gtt att 1171
Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe Lys His Gly Val Ile
345 350 355

ttg aat gca ccg gcg gac aac att atc cgt ttg acc ccg ccg ctg gtg 1219
Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu Thr Pro Pro Leu Val
360 365 370

atc acc gac gaa gaa atc gca gac gca gtc aag gct att gcc gag aca 1267
Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys Ala Ile Ala Glu Thr
375 380 385

atc gca taaaggactc aaacttatga ctt 1296
Ile Ala
390

<210> 58
<211> 391
<212> PRT
<213> Corynebacterium glutamicum

<400> 58
Met Ser Thr Leu Glu Thr Trp Pro Gln Val Ile Ile Asn Thr Tyr Gly
1 5 10 15

Thr Pro Pro Val Glu Leu Val Ser Gly Lys Gly Ala Thr Val Thr Asp
20 25 30

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Asp Gln Gly Asn Val Tyr Ile Asp Leu Leu Ala Gly Ile Ala Val Asn
        35                  40                  45

Ala Leu Gly His Ala His Pro Ala Ile Ile Glu Ala Val Thr Asn Gln
    50                  55                  60

Ile Gly Gln Leu Gly His Val Ser Asn Leu Phe Ala Ser Arg Pro Val
65                  70                  75                  80

Val Glu Val Ala Glu Glu Leu Ile Lys Arg Phe Ser Leu Asp Asp Ala
                85                  90                  95

Thr Leu Ala Ala Gln Thr Arg Val Phe Phe Cys Asn Ser Gly Ala Glu
            100                 105                 110

Ala Asn Glu Ala Ala Phe Lys Ile Ala Arg Leu Thr Gly Arg Ser Arg
        115                 120                 125

Ile Leu Ala Ala Val His Gly Phe His Gly Arg Thr Met Gly Ser Leu
    130                 135                 140

Ala Leu Thr Gly Gln Pro Asp Lys Arg Glu Ala Phe Leu Pro Met Pro
145                 150                 155                 160

Ser Gly Val Glu Phe Tyr Pro Tyr Gly Asp Thr Asp Tyr Leu Arg Lys
                165                 170                 175

Met Val Glu Thr Asn Pro Thr Asp Val Ala Ala Ile Phe Leu Glu Pro
            180                 185                 190

Ile Gln Gly Glu Thr Gly Val Val Pro Ala Pro Glu Gly Phe Leu Lys
        195                 200                 205

Ala Val Arg Glu Leu Cys Asp Glu Tyr Gly Ile Leu Met Ile Thr Asp
    210                 215                 220

Glu Val Gln Thr Gly Val Gly Arg Thr Gly Asp Phe Phe Ala His Gln
225                 230                 235                 240

His Asp Gly Val Val Pro Asp Val Val Thr Met Ala Lys Gly Leu Gly
                245                 250                 255

Gly Gly Leu Pro Ile Gly Ala Cys Leu Ala Thr Gly Arg Ala Ala Glu
            260                 265                 270

Leu Met Thr Pro Gly Lys His Gly Thr Thr Phe Gly Gly Asn Pro Val
        275                 280                 285

Ala Cys Ala Ala Ala Lys Ala Val Leu Ser Val Val Asp Asp Ala Phe
    290                 295                 300

Cys Ala Glu Val Ala Arg Lys Gly Glu Leu Phe Lys Glu Leu Leu Ala
305                 310                 315                 320

Lys Val Asp Gly Val Val Asp Val Arg Gly Arg Gly Leu Met Leu Gly
                325                 330                 335

Val Val Leu Glu Arg Asp Val Ala Lys Gln Ala Val Leu Asp Gly Phe
            340                 345                 350
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Lys His Gly Val Ile Leu Asn Ala Pro Ala Asp Asn Ile Ile Arg Leu
        355                 360                 365

Thr Pro Pro Leu Val Ile Thr Asp Glu Glu Ile Ala Asp Ala Val Lys
    370                 375                 380

Ala Ile Ala Glu Thr Ile Ala
385                 390


<210> 59
<211> 1008
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(985)
<223> RXC00733

<400> 59
acggcgaggt tgtcggtatt ggaacgcaca cgaatttgct gaacacgtgc ggtacctacc 60

gtgaaattgt tgaatcccaa gagactgcgc aggcgcaatc atg agt aat act gca    115
                                            Met Ser Asn Thr Ala
                                            1               5

ggc ccc cgc ggg cgt tcc cat cag gca gac gcc gcg ccg aat caa aag    163
Gly Pro Arg Gly Arg Ser His Gln Ala Asp Ala Ala Pro Asn Gln Lys
                10                  15                  20

gca cag aat ttc gga cca tct gcc aaa agg ctt ttc gga att cta ggc    211
Ala Gln Asn Phe Gly Pro Ser Ala Lys Arg Leu Phe Gly Ile Leu Gly
            25                  30                  35

cat gac cgt aac acc tta att ttt gtt atc ttc cta gcc gtc ctg agc    259
His Asp Arg Asn Thr Leu Ile Phe Val Ile Phe Leu Ala Val Leu Ser
        40                  45                  50

gtt gga ctt acc gtc ttg ggc cca tgg ttg ctg ggt aaa gcc acc aac    307
Val Gly Leu Thr Val Leu Gly Pro Trp Leu Leu Gly Lys Ala Thr Asn
    55                  60                  65

gtg gtg ttt gaa gga ttc cta tct aag cgc atg ccg gct ggt gcg tca    355
Val Val Phe Glu Gly Phe Leu Ser Lys Arg Met Pro Ala Gly Ala Ser
70                  75                  80                  85

aag gaa gat atc atc gcg cag ttg cag gct gca ggt aaa cat aat cag    403
Lys Glu Asp Ile Ile Ala Gln Leu Gln Ala Ala Gly Lys His Asn Gln
                90                  95                  100

gct tcc atg atg gaa gac atg aac ctt gtt cca ggc tca ggc att gat    451
Ala Ser Met Met Glu Asp Met Asn Leu Val Pro Gly Ser Gly Ile Asp
            105                 110                 115

ttt gaa aaa tta gcc atg atc ctc gga ctg gtg atc ggt gct tat ctc    499
Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val Ile Gly Ala Tyr Leu
        120                 125                 130

atc ggt agc ctg ttg tcg ttg ttc cag gcg cgg atg ctc aac cgc atc    547
Ile Gly Ser Leu Leu Ser Leu Phe Gln Ala Arg Met Leu Asn Arg Ile
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135 140 145

gtg caa agt gcc atg cac cgg ctg cgc atg gag gtg gag gaa aaa atc 595
Val Gln Ser Ala Met His Arg Leu Arg Met Glu Val Glu Glu Lys Ile
150 155 160 165

cac cgc cta ccg ctg agc tat ttc gat tcc atc aaa cgt ggt gat ctg 643
His Arg Leu Pro Leu Ser Tyr Phe Asp Ser Ile Lys Arg Gly Asp Leu
170 175 180

ctt agc cgt gtg acc aac gat gtg gat aat atc ggt caa tcc ctg caa 691
Leu Ser Arg Val Thr Asn Asp Val Asp Asn Ile Gly Gln Ser Leu Gln
185 190 195

caa acc ttg tca cag gcg atc act tcc cta ctg acc gtc atc ggt gtg 739
Gln Thr Leu Ser Gln Ala Ile Thr Ser Leu Leu Thr Val Ile Gly Val
200 205 210

ttg gtg atg atg ttt atc atc tcc cca ctg ctc gca ctc gtg gcg ctg 787
Leu Val Met Met Phe Ile Ile Ser Pro Leu Leu Ala Leu Val Ala Leu
215 220 225

gta tcc att ccg gtc acc atc gtg gtc act gtg gtg gtt gcg agc cgt 835
Val Ser Ile Pro Val Thr Ile Val Val Thr Val Val Val Ala Ser Arg
230 235 240 245

tcc cag aaa ctc ttt gcg gaa cag tgg aag cag acc ggt att ttg aat 883
Ser Gln Lys Leu Phe Ala Glu Gln Trp Lys Gln Thr Gly Ile Leu Asn
250 255 260

gcg cgc ctg gag gaa acc tac tct ggc cac gcc gtg gtt aag gtt ttc 931
Ala Arg Leu Glu Glu Thr Tyr Ser Gly His Ala Val Val Lys Val Phe
265 270 275

gga cac caa aag gat gtt caa gaa gca ttc gag gaa gaa aat caa gct 979
Gly His Gln Lys Asp Val Gln Glu Ala Phe Glu Glu Glu Asn Gln Ala
280 285 290

tgt gta taaggccagc tttggtgccc agt 1008
Cys Val
295

<210> 60
<211> 295
<212> PRT
<213> Corynebacterium glutamicum

<400> 60
Met Ser Asn Thr Ala Gly Pro Arg Gly Arg Ser His Gln Ala Asp Ala
1 5 10 15

Ala Pro Asn Gln Lys Ala Gln Asn Phe Gly Pro Ser Ala Lys Arg Leu
20 25 30

Phe Gly Ile Leu Gly His Asp Arg Asn Thr Leu Ile Phe Val Ile Phe
35 40 45

Leu Ala Val Leu Ser Val Gly Leu Thr Val Leu Gly Pro Trp Leu Leu
50 55 60

```
Gly Lys Ala Thr Asn Val Val Phe Glu Gly Phe Leu Ser Lys Arg Met
 65                  70                  75                  80

Pro Ala Gly Ala Ser Lys Glu Asp Ile Ile Ala Gln Leu Gln Ala Ala
                 85                  90                  95

Gly Lys His Asn Gln Ala Ser Met Met Glu Asp Met Asn Leu Val Pro
            100                 105                 110

Gly Ser Gly Ile Asp Phe Glu Lys Leu Ala Met Ile Leu Gly Leu Val
        115                 120                 125

Ile Gly Ala Tyr Leu Ile Gly Ser Leu Leu Ser Leu Phe Gln Ala Arg
    130                 135                 140

Met Leu Asn Arg Ile Val Gln Ser Ala Met His Arg Leu Arg Met Glu
145                 150                 155                 160

Val Glu Glu Lys Ile His Arg Leu Pro Leu Ser Tyr Phe Asp Ser Ile
                165                 170                 175

Lys Arg Gly Asp Leu Leu Ser Arg Val Thr Asn Asp Val Asp Asn Ile
            180                 185                 190

Gly Gln Ser Leu Gln Gln Thr Leu Ser Gln Ala Ile Thr Ser Leu Leu
        195                 200                 205

Thr Val Ile Gly Val Leu Val Met Met Phe Ile Ile Ser Pro Leu Leu
    210                 215                 220

Ala Leu Val Ala Leu Val Ser Ile Pro Val Thr Ile Val Val Thr Val
225                 230                 235                 240

Val Val Ala Ser Arg Ser Gln Lys Leu Phe Ala Glu Gln Trp Lys Gln
                245                 250                 255

Thr Gly Ile Leu Asn Ala Arg Leu Glu Glu Thr Tyr Ser Gly His Ala
            260                 265                 270

Val Val Lys Val Phe Gly His Gln Lys Asp Val Gln Glu Ala Phe Glu
        275                 280                 285

Glu Glu Asn Gln Ala Cys Val
    290                 295
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<210> 61
<211> 426
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(426)
<223> RXC00861

<400> 61
atg gct cct cac aag gtc atg ctg att acc act ggt act cag ggt gag 48
Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
  1   5   10   15

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cct atg gct gcg ctg tct cgc atg gcg cgt cgt gag cac cga cag atc       96
Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
            20                  25                  30

act gtc cgt gat gga gac ttg att atc ctt tct tcc tcc ctg gtt cca      144
Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
        35                  40                  45

ggt aac gaa gaa gca gtg ttc ggt gtc atc aac atg ctg gct cag atc      192
Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
    50                  55                  60

ggt gca act gtt gtt acc ggt cgc gac gcc aag gtg cac acc tcg ggc      240
Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
65                  70                  75                      80

cac ggc tac tcc gga gag ctg ttg ttc ttg tac aac gcc gct cgt ccg      288
His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro
                85                  90                  95

aag aac gct atg cct gtc cac ggc gag tgg cgc cac ctg cgc gcc aac      336
Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn
            100                 105                 110

aag gaa ctg gct atc tcc act ggt gtt aac cgc gac aac gtt gtg ctt      384
Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu
        115                 120                 125

gca caa aac ggt gtt gtg gtt gat atg gtc aac ggt cgc gca              426
Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala
    130                 135                 140


<210> 62
<211> 142
<212> PRT
<213> Corynebacterium glutamicum

<400> 62
Met Ala Pro His Lys Val Met Leu Ile Thr Thr Gly Thr Gln Gly Glu
1               5                   10                  15

Pro Met Ala Ala Leu Ser Arg Met Ala Arg Arg Glu His Arg Gln Ile
            20                  25                  30

Thr Val Arg Asp Gly Asp Leu Ile Ile Leu Ser Ser Ser Leu Val Pro
        35                  40                  45

Gly Asn Glu Glu Ala Val Phe Gly Val Ile Asn Met Leu Ala Gln Ile
    50                  55                  60

Gly Ala Thr Val Val Thr Gly Arg Asp Ala Lys Val His Thr Ser Gly
65                  70                  75                      80

His Gly Tyr Ser Gly Glu Leu Leu Phe Leu Tyr Asn Ala Ala Arg Pro
                85                  90                  95

Lys Asn Ala Met Pro Val His Gly Glu Trp Arg His Leu Arg Ala Asn
            100                 105                 110

Lys Glu Leu Ala Ile Ser Thr Gly Val Asn Arg Asp Asn Val Val Leu
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115 120 125

Ala Gln Asn Gly Val Val Val Asp Met Val Asn Gly Arg Ala
130 135 140

<210> 63
<211> 1066
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1066)
<223> RXC00866

<400> 63
gcatcaacgt aggagatcct cgacttccaa ttatggctcc aaatgagcag gaacttgagg 60

ctctccgaga agacatgaaa aaagctggag ttctataaat atg aat gat tcc cga 115
Met Asn Asp Ser Arg
1 5

aat cgc ggc cgg aag gtt acc cgc aag gcg ggc cca cca gaa gct ggt 163
Asn Arg Gly Arg Lys Val Thr Arg Lys Ala Gly Pro Pro Glu Ala Gly
10 15 20

cag gaa aac cat ctg gat acc cct gtc ttt cag gca cca gat gct tcc 211
Gln Glu Asn His Leu Asp Thr Pro Val Phe Gln Ala Pro Asp Ala Ser
25 30 35

tct aac cag agc gct gta aaa gct gag acc gcc gga aac gac aat cgg 259
Ser Asn Gln Ser Ala Val Lys Ala Glu Thr Ala Gly Asn Asp Asn Arg
40 45 50

gat gct gcg caa ggt gct caa gga tcc caa gat tct cag ggt tcc cag 307
Asp Ala Ala Gln Gly Ala Gln Gly Ser Gln Asp Ser Gln Gly Ser Gln
55 60 65

aac gct caa ggt tcc cag aac cgc gag tcc gga aac aac aac cgc aac 355
Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly Asn Asn Asn Arg Asn
70 75 80 85

cgt tcc aac aac aac cgt cgc ggt ggt cgt gga cgt cgt gga tcc gga 403
Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly Arg Arg Gly Ser Gly
90 95 100

aac gcc aat gag ggc gcg aac aac aac agc ggt aac cag aac cgt cag 451
Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly Asn Gln Asn Arg Gln
105 110 115

ggc gga aac cgt ggc aac cgc ggt ggc gga cgc cga aac gtt gtt aag 499
Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg Arg Asn Val Val Lys
120 125 130

tcg atg cag ggt gcg gat ctg acc cag cgc ctg cca gag cca cca aag 547
Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu Pro Glu Pro Pro Lys
135 140 145

gca ccg gca aac ggt ctg cgt att tac gca ctt ggt ggc att tcc gaa 595
Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu Gly Gly Ile Ser Glu

150 155 160 165

atc ggt cgc aac atg acc gtg ttt gag tac aac aac cgt ctg ctc atc 643
Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn Asn Arg Leu Leu Ile
170 175 180

gtg gac tgt ggt gtg ctc ttc cca tct tca ggt gag cca ggc gtt gac 691
Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly Glu Pro Gly Val Asp
185 190 195

ctg att ctt cct gac ttc ggc cca att gag gat cac ctg cac cgc gtc 739
Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp His Leu His Arg Val
200 205 210

gat gca ttg gtg gtt act cac gga cac gaa gac cac att ggt gct att 787
Asp Ala Leu Val Val Thr His Gly His Glu Asp His Ile Gly Ala Ile
215 220 225

ccc tgg ctg ctg aag ctg cgc aac gat atc cca atc ttg gca tcc cgt 835
Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro Ile Leu Ala Ser Arg
230 235 240 245

ttc acc ttg gct ctg att gca gct aag tgt aag gaa cac cgt cag cgt 883
Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys Glu His Arg Gln Arg
250 255 260

ccg aag ctg atc gag gtc aac gag cag tcc aat gag gac cgc gga ccg 931
Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn Glu Asp Arg Gly Pro
265 270 275

ttc aac att cgc ttc tgg gct gtt aac cac tcc atc cca gac tgc ctt 979
Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser Ile Pro Asp Cys Leu
280 285 290

ggt ctt gct atc aag act cct gct ggt ttg gtc atc cac acc ggt gac 1027
Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val Ile His Thr Gly Asp
295 300 305

atc aag ctg gat cag act cct cct gat gga cgc cca act 1066
Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg Pro Thr
310 315 320

<210> 64
<211> 322
<212> PRT
<213> Corynebacterium glutamicum

<400> 64
Met Asn Asp Ser Arg Asn Arg Gly Arg Lys Val Thr Arg Lys Ala Gly
1 5 10 15

Pro Pro Glu Ala Gly Gln Glu Asn His Leu Asp Thr Pro Val Phe Gln
20 25 30

Ala Pro Asp Ala Ser Ser Asn Gln Ser Ala Val Lys Ala Glu Thr Ala
35 40 45

Gly Asn Asp Asn Arg Asp Ala Ala Gln Gly Ala Gln Gly Ser Gln Asp
50 55 60

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Ser Gln Gly Ser Gln Asn Ala Gln Gly Ser Gln Asn Arg Glu Ser Gly
 65                  70                  75                  80

Asn Asn Asn Arg Asn Arg Ser Asn Asn Asn Arg Arg Gly Gly Arg Gly
                 85                  90                  95

Arg Arg Gly Ser Gly Asn Ala Asn Glu Gly Ala Asn Asn Asn Ser Gly
            100                 105                 110

Asn Gln Asn Arg Gln Gly Gly Asn Arg Gly Asn Arg Gly Gly Gly Arg
        115                 120                 125

Arg Asn Val Val Lys Ser Met Gln Gly Ala Asp Leu Thr Gln Arg Leu
    130                 135                 140

Pro Glu Pro Pro Lys Ala Pro Ala Asn Gly Leu Arg Ile Tyr Ala Leu
145                 150                 155                 160

Gly Gly Ile Ser Glu Ile Gly Arg Asn Met Thr Val Phe Glu Tyr Asn
                165                 170                 175

Asn Arg Leu Leu Ile Val Asp Cys Gly Val Leu Phe Pro Ser Ser Gly
            180                 185                 190

Glu Pro Gly Val Asp Leu Ile Leu Pro Asp Phe Gly Pro Ile Glu Asp
        195                 200                 205

His Leu His Arg Val Asp Ala Leu Val Val Thr His Gly His Glu Asp
    210                 215                 220

His Ile Gly Ala Ile Pro Trp Leu Leu Lys Leu Arg Asn Asp Ile Pro
225                 230                 235                 240

Ile Leu Ala Ser Arg Phe Thr Leu Ala Leu Ile Ala Ala Lys Cys Lys
                245                 250                 255

Glu His Arg Gln Arg Pro Lys Leu Ile Glu Val Asn Glu Gln Ser Asn
            260                 265                 270

Glu Asp Arg Gly Pro Phe Asn Ile Arg Phe Trp Ala Val Asn His Ser
        275                 280                 285

Ile Pro Asp Cys Leu Gly Leu Ala Ile Lys Thr Pro Ala Gly Leu Val
    290                 295                 300

Ile His Thr Gly Asp Ile Lys Leu Asp Gln Thr Pro Pro Asp Gly Arg
305                 310                 315                 320

Pro Thr
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<210> 65
<211> 1527
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1504)
<223> RXC02095

<400> 65
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tactccccca acaggctcaa aaatactgaa aggctcacgc atg aaa act gag caa 115
Met Lys Thr Glu Gln
1 5

tcc caa aaa gca caa tta gcc cct aag aaa gca cct gaa aag cca caa 163
Ser Gln Lys Ala Gln Leu Ala Pro Lys Lys Ala Pro Glu Lys Pro Gln
10 15 20

cgc atc cgc caa ctt att tcc gtg gcg tgg cag cga cct tgg ctc acc 211
Arg Ile Arg Gln Leu Ile Ser Val Ala Trp Gln Arg Pro Trp Leu Thr
25 30 35

tca ttc acc gta atc agc gct tta gct gca acg ttg ttt gaa ctt aca 259
Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr Leu Phe Glu Leu Thr
40 45 50

ctt cct ctt ttg acc ggt ggc gcc atc gat atc gcg ctc gga aat acc 307
Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile Ala Leu Gly Asn Thr
55 60 65

gga gat act tta acc act gac ctg ctg gac cgg ttc act ccg agt gga 355
Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg Phe Thr Pro Ser Gly
70 75 80 85

tta agc gtg ttg acc agc gtc att gcc ctt atc gtg ctt ctc gcg ttg 403
Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile Val Leu Leu Ala Leu
90 95 100

ctt cgc tat gcc agt caa ttt gga cgg cga tac acc gca ggc aag ctc 451
Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr Thr Ala Gly Lys Leu
105 110 115

agc atg ggg gta cag cat gat gtc cgg ctt aaa acg atg cgc tca ttg 499
Ser Met Gly Val Gln His Asp Val Arg Leu Lys Thr Met Arg Ser Leu
120 125 130

cag aac ctc gat ggg cca ggt cag gac tct att cgc aca ggc caa gta 547
Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile Arg Thr Gly Gln Val
135 140 145

gtc agt cgg tcc att tcg gat atc aac atg gtg caa agc ctt gtg gcg 595
Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val Gln Ser Leu Val Ala
150 155 160 165

atg ttg ccg atg ttg atc gga aat gtg gtc aag ctt gtg ctc act ttg 643
Met Leu Pro Met Leu Ile Gly Asn Val Val Lys Leu Val Leu Thr Leu
170 175 180

gtg atc atg ctg gct att tcc ccg ccg ctg acc atc atc gct gca gtg 691
Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr Ile Ile Ala Ala Val
185 190 195

ttg gtg cct ttg ctg ttg tgg gcc gtg gcc tat tcg cga aaa gcg ctt 739
Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr Ser Arg Lys Ala Leu
200 205 210

ttt gcg tcc acg tgg tcg gcc cag caa aag gct gcg gat ctg acc act 787

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Phe Ala Ser Thr Trp Ser Ala Gln Gln Lys Ala Ala Asp Leu Thr Thr
    215                 220                 225

cat gtg gaa gaa act gtc acg ggt atc cgc gtg gtc aag gca ttt gcg      835
His Val Glu Glu Thr Val Thr Gly Ile Arg Val Val Lys Ala Phe Ala
230                 235                 240                 245

cag gaa gac cgc gag acc gac aaa ttg gat ctc acc gca cgt gag tta      883
Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu Thr Ala Arg Glu Leu
                250                 255                 260

ttt gcc cag cgc atg cgc act gca cgt ctg acg gca aag ttc atc ccc      931
Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr Ala Lys Phe Ile Pro
            265                 270                 275

atg gtt gag cag ctt ccg cag ctt gct ttg gtg gtc aac att gtt ggc      979
Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val Val Asn Ile Val Gly
        280                 285                 290

ggt ggc tat ttg gcc atg act ggt cac atc acg gtg ggc acg ttt gtg      1027
Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr Val Gly Thr Phe Val
    295                 300                 305

gcg ttt tct tcc tat ctc act agc ttg tcg gcg gtg gct agg tcc ctg      1075
Ala Phe Ser Ser Tyr Leu Thr Ser Leu Ser Ala Val Ala Arg Ser Leu
310                 315                 320                 325

tcg ggc atg ctc atg cgc gtg cag ttg gcg ctg tct tct gtg gag cgc      1123
Ser Gly Met Leu Met Arg Val Gln Leu Ala Leu Ser Ser Val Glu Arg
                330                 335                 340

atc ttt gaa gtc att gat ctt cag cct gaa cgc acc gat cct gca cac      1171
Ile Phe Glu Val Ile Asp Leu Gln Pro Glu Arg Thr Asp Pro Ala His
            345                 350                 355

ccc ctg tca ctt ccc gac act ccc ctg ggt ctg tcg ttc aac aac gta      1219
Pro Leu Ser Leu Pro Asp Thr Pro Leu Gly Leu Ser Phe Asn Asn Val
        360                 365                 370

gat ttc cgt ggg att ctc aac ggt ttt gag ctg ggt gtt cag gcc ggt      1267
Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu Gly Val Gln Ala Gly
    375                 380                 385

gaa acc gtt gtg ttg gtg ggc cct cca ggt tca ggc aag acc atg gct      1315
Glu Thr Val Val Leu Val Gly Pro Pro Gly Ser Gly Lys Thr Met Ala
390                 395                 400                 405

gtg cag ctt gct gga aac ttt tat caa cca gac agc ggc cac atc gcc      1363
Val Gln Leu Ala Gly Asn Phe Tyr Gln Pro Asp Ser Gly His Ile Ala
                410                 415                 420

ttt gat agc aac ggc cat cgc act cgc ttc gac gac ctc acc cac agc      1411
Phe Asp Ser Asn Gly His Arg Thr Arg Phe Asp Asp Leu Thr His Ser
            425                 430                 435

gat atc cgc agg aat ctc atc gcg gtt ttt gat gag ccg ttc ttg tac      1459
Asp Ile Arg Arg Asn Leu Ile Ala Val Phe Asp Glu Pro Phe Leu Tyr
        440                 445                 450

tcc tcc tcc ata ccg cga gaa cat ctc gat ggg ttt gga tgt cag          1504
Ser Ser Ser Ile Pro Arg Glu His Leu Asp Gly Phe Gly Cys Gln
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455 460 465

tgatgagcag atcgaacacg cag 1527

<210> 66
<211> 468
<212> PRT
<213> Corynebacterium glutamicum

<400> 66
Met Lys Thr Glu Gln Ser Gln Lys Ala Gln Leu Ala Pro Lys Lys Ala
1 5 10 15

Pro Glu Lys Pro Gln Arg Ile Arg Gln Leu Ile Ser Val Ala Trp Gln
20 25 30

Arg Pro Trp Leu Thr Ser Phe Thr Val Ile Ser Ala Leu Ala Ala Thr
35 40 45

Leu Phe Glu Leu Thr Leu Pro Leu Leu Thr Gly Gly Ala Ile Asp Ile
50 55 60

Ala Leu Gly Asn Thr Gly Asp Thr Leu Thr Thr Asp Leu Leu Asp Arg
65 70 75 80

Phe Thr Pro Ser Gly Leu Ser Val Leu Thr Ser Val Ile Ala Leu Ile
85 90 95

Val Leu Leu Ala Leu Leu Arg Tyr Ala Ser Gln Phe Gly Arg Arg Tyr
100 105 110

Thr Ala Gly Lys Leu Ser Met Gly Val Gln His Asp Val Arg Leu Lys
115 120 125

Thr Met Arg Ser Leu Gln Asn Leu Asp Gly Pro Gly Gln Asp Ser Ile
130 135 140

Arg Thr Gly Gln Val Val Ser Arg Ser Ile Ser Asp Ile Asn Met Val
145 150 155 160

Gln Ser Leu Val Ala Met Leu Pro Met Leu Ile Gly Asn Val Val Lys
165 170 175

Leu Val Leu Thr Leu Val Ile Met Leu Ala Ile Ser Pro Pro Leu Thr
180 185 190

Ile Ile Ala Ala Val Leu Val Pro Leu Leu Leu Trp Ala Val Ala Tyr
195 200 205

Ser Arg Lys Ala Leu Phe Ala Ser Thr Trp Ser Ala Gln Gln Lys Ala
210 215 220

Ala Asp Leu Thr Thr His Val Glu Glu Thr Val Thr Gly Ile Arg Val
225 230 235 240

Val Lys Ala Phe Ala Gln Glu Asp Arg Glu Thr Asp Lys Leu Asp Leu
245 250 255

Thr Ala Arg Glu Leu Phe Ala Gln Arg Met Arg Thr Ala Arg Leu Thr
260 265 270

Ala Lys Phe Ile Pro Met Val Glu Gln Leu Pro Gln Leu Ala Leu Val
275 280 285

Val Asn Ile Val Gly Gly Gly Tyr Leu Ala Met Thr Gly His Ile Thr
290 295 300

Val Gly Thr Phe Val Ala Phe Ser Ser Tyr Leu Thr Ser Leu Ser Ala
305 310 315 320

Val Ala Arg Ser Leu Ser Gly Met Leu Met Arg Val Gln Leu Ala Leu
325 330 335

Ser Ser Val Glu Arg Ile Phe Glu Val Ile Asp Leu Gln Pro Glu Arg
340 345 350

Thr Asp Pro Ala His Pro Leu Ser Leu Pro Asp Thr Pro Leu Gly Leu
355 360 365

Ser Phe Asn Asn Val Asp Phe Arg Gly Ile Leu Asn Gly Phe Glu Leu
370 375 380

Gly Val Gln Ala Gly Glu Thr Val Val Leu Val Gly Pro Pro Gly Ser
385 390 395 400

Gly Lys Thr Met Ala Val Gln Leu Ala Gly Asn Phe Tyr Gln Pro Asp
405 410 415

Ser Gly His Ile Ala Phe Asp Ser Asn Gly His Arg Thr Arg Phe Asp
420 425 430

Asp Leu Thr His Ser Asp Ile Arg Arg Asn Leu Ile Ala Val Phe Asp
435 440 445

Glu Pro Phe Leu Tyr Ser Ser Ser Ile Pro Arg Glu His Leu Asp Gly
450 455 460

Phe Gly Cys Gln
465

<210> 67
<211> 295
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (84)..(272)
<223> RXC03185

<400> 67
agcgcccaac cgttcagacc agcggtttct ctgaggatgc aaagtccatg atgggtnagg 60

tcactgagct gtccgaaacc acc atg aat gat ctt gca gct gaa ggt gaa aac 113
Met Asn Asp Leu Ala Ala Glu Gly Glu Asn
1 5 10

gat cct tac cgc atg gtt cag cag ctg cgc cgc aag ctc tct cgc ttc 161
Asp Pro Tyr Arg Met Val Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe
15 20 25

gtc gag cag aag tgg aag cgc cag ccg gtc atc atg cca acc gtc att 209
Val Glu Gln Lys Trp Lys Arg Gln Pro Val Ile Met Pro Thr Val Ile
30 35 40

ccg atg act gcg gaa acc acg cac atc ggt gac gat gag gtt cgc gct 257
Pro Met Thr Ala Glu Thr Thr His Ile Gly Asp Asp Glu Val Arg Ala
45 50 55

tca cgc gag tcc ctg taaaagcatt tcgcttttcg acg 295
Ser Arg Glu Ser Leu
60

<210> 68
<211> 63
<212> PRT
<213> Corynebacterium glutamicum

<400> 68
Met Asn Asp Leu Ala Ala Glu Gly Glu Asn Asp Pro Tyr Arg Met Val
1 5 10 15

Gln Gln Leu Arg Arg Lys Leu Ser Arg Phe Val Glu Gln Lys Trp Lys
20 25 30

Arg Gln Pro Val Ile Met Pro Thr Val Ile Pro Met Thr Ala Glu Thr
35 40 45

Thr His Ile Gly Asp Asp Glu Val Arg Ala Ser Arg Glu Ser Leu
50 55 60

<210> 69
<211> 1170
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1147)
<223> RXA00115

<400> 69
tggattctcg agtctgtaca cccttgatca aagcccgagt gttccgtaga ttaactttgt 60

cgtatattgt gacctacacc ccatactgtt aggagttttc atg ctc gac aat agt 115
Met Leu Asp Asn Ser
1 5

ttt tac acc gca gag gtt cag ggc cca tac gaa acc gct tcc att ggc 163
Phe Tyr Thr Ala Glu Val Gln Gly Pro Tyr Glu Thr Ala Ser Ile Gly
10 15 20

cgg ctc gaa ctc gaa gaa ggg ggt gtg att gag gat tgc tgg ttg gct 211
Arg Leu Glu Leu Glu Glu Gly Gly Val Ile Glu Asp Cys Trp Leu Ala
25 30 35

tac gct aca gct gga acg ctc aac gag gac aag tcc aac gcc atc ctc 259
Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys Ser Asn Ala Ile Leu
40 45 50

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att ccg acg tgg tac tcc gga acc cat cag acc tgg ttc cag cag tac     307
Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr Trp Phe Gln Gln Tyr
     55                  60                  65

atc ggc act gat cat gcg ctg gat cca tca aag tat ttc atc atc tcc     355
Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys Tyr Phe Ile Ile Ser
 70                  75                  80                  85

atc aac caa atc ggt aat ggt ttg tcg gtc tcc cct gcc aac acg gct     403
Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser Pro Ala Asn Thr Ala
                 90                  95                 100

gat gac agc atc tcg atg tcc aag ttc ccg aat gtt cgc att ggt gat     451
Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn Val Arg Ile Gly Asp
            105                 110                 115

gat gtc gtt gcc cag gac cgg ctc ttg cgc caa gag ttt ggt att acc     499
Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln Glu Phe Gly Ile Thr
        120                 125                 130

gag ctc ttt gcc gtc gtt ggt ggt tcg atg ggt gcg cag caa acc tat     547
Glu Leu Phe Ala Val Val Gly Gly Ser Met Gly Ala Gln Gln Thr Tyr
    135                 140                 145

gag tgg att gtt cgc ttc cct gac caa gtt cat cga gca gct ccg atc     595
Glu Trp Ile Val Arg Phe Pro Asp Gln Val His Arg Ala Ala Pro Ile
150                 155                 160                 165

gcg ggc act gcg aag aac act cct cat gat ttc atc ttc acc cag act     643
Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe Ile Phe Thr Gln Thr
                170                 175                 180

ctt aat gag acc gtt gag gcc gat cca ggg ttc aat ggc ggc gaa tac     691
Leu Asn Glu Thr Val Glu Ala Asp Pro Gly Phe Asn Gly Gly Glu Tyr
            185                 190                 195

tcc tcc cat gaa gag gta gct gat gga ctt cgc cgt caa tcg cat ctt     739
Ser Ser His Glu Glu Val Ala Asp Gly Leu Arg Arg Gln Ser His Leu
        200                 205                 210

tgg gct gcc atg gga ttt tcc aca gag ttc tgg aag cag gag gca tgg     787
Trp Ala Ala Met Gly Phe Ser Thr Glu Phe Trp Lys Gln Glu Ala Trp
    215                 220                 225

cgt cgc ctg gga ctt gaa agt aag gag tca gtg ctc gcg gac ttc ctg     835
Arg Arg Leu Gly Leu Glu Ser Lys Glu Ser Val Leu Ala Asp Phe Leu
230                 235                 240                 245

gat ccg ctg ttc atg tcc atg gat cct aat acc ttg ctc aac aac gct     883
Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr Leu Leu Asn Asn Ala
                250                 255                 260

tgg aag tgg cag cat ggc gat gtc tct cgc cac acc ggc ggc gac ttg     931
Trp Lys Trp Gln His Gly Asp Val Ser Arg His Thr Gly Gly Asp Leu
            265                 270                 275

gca gcg gct ctt ggc cga gtg aag gct aag acc ttc gtt atg ccc atc     979
Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr Phe Val Met Pro Ile
        280                 285                 290
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agc gag gac atg ttc ttt cct gtt cgt gac tgt gcc gca gaa caa gca 1027
Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys Ala Ala Glu Gln Ala
295 300 305

ctc atc cca ggc agc gag ctt cga gtg atc gaa gac atc gcc ggt cac 1075
Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu Asp Ile Ala Gly His
310 315 320 325

ctt ggg ctt ttt aac gtc tct gag aat tac atc cca cag atc gac aaa 1123
Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile Pro Gln Ile Asp Lys
330 335 340

aat ctg aaa gag ctg ttc gag agc taaacactga tgtcaaagag cct 1170
Asn Leu Lys Glu Leu Phe Glu Ser
345

<210> 70
<211> 349
<212> PRT
<213> Corynebacterium glutamicum

<400> 70
Met Leu Asp Asn Ser Phe Tyr Thr Ala Glu Val Gln Gly Pro Tyr Glu
1 5 10 15

Thr Ala Ser Ile Gly Arg Leu Glu Leu Glu Glu Gly Gly Val Ile Glu
20 25 30

Asp Cys Trp Leu Ala Tyr Ala Thr Ala Gly Thr Leu Asn Glu Asp Lys
35 40 45

Ser Asn Ala Ile Leu Ile Pro Thr Trp Tyr Ser Gly Thr His Gln Thr
50 55 60

Trp Phe Gln Gln Tyr Ile Gly Thr Asp His Ala Leu Asp Pro Ser Lys
65 70 75 80

Tyr Phe Ile Ile Ser Ile Asn Gln Ile Gly Asn Gly Leu Ser Val Ser
85 90 95

Pro Ala Asn Thr Ala Asp Asp Ser Ile Ser Met Ser Lys Phe Pro Asn
100 105 110

Val Arg Ile Gly Asp Asp Val Val Ala Gln Asp Arg Leu Leu Arg Gln
115 120 125

Glu Phe Gly Ile Thr Glu Leu Phe Ala Val Val Gly Gly Ser Met Gly
130 135 140

Ala Gln Gln Thr Tyr Glu Trp Ile Val Arg Phe Pro Asp Gln Val His
145 150 155 160

Arg Ala Ala Pro Ile Ala Gly Thr Ala Lys Asn Thr Pro His Asp Phe
165 170 175

Ile Phe Thr Gln Thr Leu Asn Glu Thr Val Glu Ala Asp Pro Gly Phe
180 185 190

Asn Gly Gly Glu Tyr Ser Ser His Glu Glu Val Ala Asp Gly Leu Arg
195 200 205

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Arg Gln Ser His Leu Trp Ala Ala Met Gly Phe Ser Thr Glu Phe Trp
    210                 215                 220

Lys Gln Glu Ala Trp Arg Arg Leu Gly Leu Glu Ser Lys Glu Ser Val
225                 230                 235                 240

Leu Ala Asp Phe Leu Asp Pro Leu Phe Met Ser Met Asp Pro Asn Thr
                245                 250                 255

Leu Leu Asn Asn Ala Trp Lys Trp Gln His Gly Asp Val Ser Arg His
            260                 265                 270

Thr Gly Gly Asp Leu Ala Ala Ala Leu Gly Arg Val Lys Ala Lys Thr
        275                 280                 285

Phe Val Met Pro Ile Ser Glu Asp Met Phe Phe Pro Val Arg Asp Cys
    290                 295                 300

Ala Ala Glu Gln Ala Leu Ile Pro Gly Ser Glu Leu Arg Val Ile Glu
305                 310                 315                 320

Asp Ile Ala Gly His Leu Gly Leu Phe Asn Val Ser Glu Asn Tyr Ile
                325                 330                 335

Pro Gln Ile Asp Lys Asn Leu Lys Glu Leu Phe Glu Ser
            340                 345


<210> 71
<211> 1254
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1231)
<223> RXN00403

<400> 71
tttttcagac tcgtgagaat gcaaactaga ctagacagag ctgtccatat acactggacg 60

aagttttagt cttgtccacc cagaacaggc ggttattttc atg ccc acc ctc gcg   115
                                              Met Pro Thr Leu Ala
                                                1               5

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa   163
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu
                10                  15                  20

gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt   211
Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly
            25                  30                  35

gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa   259
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu
        40                  45                  50

cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg   307
His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu
    55                  60                  65
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ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt 355
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys
70 75 80 85

acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg 403
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met
90 95 100

cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att 451
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile
105 110 115

cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc 499
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile
120 125 130

acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc 547
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr
135 140 145

cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt 595
Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val
150 155 160 165

ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc 643
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser
170 175 180

gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac 691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn
185 190 195

tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga 739
Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg
200 205 210

cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc 787
Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg
215 220 225

ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc 835
Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg
230 235 240 245

aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca 883
Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala
250 255 260

gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc 931
Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr
265 270 275

gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979
Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn
280 285 290

aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat 1027
Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp
295 300 305

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac 1075
Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn
310 315 320 325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac 1123
Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His
330 335 340

gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac 1171
Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn
345 350 355

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg acc tac atc 1219
Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser Thr Tyr Ile
360 365 370

gag ttc tac atc taataggtat ttacgacaaa tag 1254
Glu Phe Tyr Ile
375

<210> 72
<211> 377
<212> PRT
<213> Corynebacterium glutamicum

<400> 72
Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly
1 5 10 15

Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
20 25 30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
35 40 45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
50 55 60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
65 70 75 80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
85 90 95

Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
100 105 110

Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
115 120 125

Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
130 135 140

Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val
145 150 155 160

Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
165 170 175

Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His

180 185 190

Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
195 200 205

Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
210 215 220

Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
225 230 235 240

Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
245 250 255

Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
260 265 270

Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
275 280 285

Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
290 295 300

Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu
305 310 315 320

His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
325 330 335

Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
340 345 350

Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
355 360 365

Pro Ser Thr Tyr Ile Glu Phe Tyr Ile
370 375

<210> 73
<211> 1210
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1210)
<223> FRXA00403

<400> 73
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aagttttagt cttgtccacc cagaacaggc ggttattttc atg ccc acc ctc gcg 115
Met Pro Thr Leu Ala
1 5

cct tca ggt caa ctt gaa atc caa gcg atc ggt gat gtc tcc acc gaa 163
Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly Asp Val Ser Thr Glu
10 15 20

gcc gga gca atc att aca aac gct gaa atc gcc tat cac cgc tgg ggt 211

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Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala Tyr His Arg Trp Gly
                25                  30                  35

gaa tac cgc gta gat aaa gaa gga cgc agc aat gtc gtt ctc atc gaa    259
Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn Val Val Leu Ile Glu
        40                  45                  50

cac gcc ctc act gga gat tcc aac gca gcc gat tgg tgg gct gac ttg    307
His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp Trp Trp Ala Asp Leu
    55                  60                  65

ctc ggt ccc ggc aaa gcc atc aac act gat att tac tgc gtg atc tgt    355
Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile Tyr Cys Val Ile Cys
 70                  75                  80                  85

acc aac gtc atc ggt ggt tgc aac ggt tcc acc gga cct ggc tcc atg    403
Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr Gly Pro Gly Ser Met
                 90                  95                 100

cat cca gat gga aat ttc tgg ggt aat cgc ttc ccc gcc acg tcc att    451
His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe Pro Ala Thr Ser Ile
            105                 110                 115

cgt gat cag gta aac gcc gaa aaa caa ttc ctc gac gca ctc ggc atc    499
Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu Asp Ala Leu Gly Ile
        120                 125                 130

acc acg gtc gcc gca gta ctt ggt ggt tcc atg ggt ggt gcc cgc acc    547
Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met Gly Gly Ala Arg Thr
    135                 140                 145

cta gag tgg gcc gca atg tac cca gaa act gtt ggc gca gct gct gtt    595
Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val Gly Ala Ala Ala Val
150                 155                 160                 165

ctt gca gtt tct gca cgc gcc agc gcc tgg caa atc ggc att caa tcc    643
Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln Ile Gly Ile Gln Ser
                170                 175                 180

gcc caa att aag gcg att gaa aac gac cac cac tgg cac gaa ggc aac    691
Ala Gln Ile Lys Ala Ile Glu Asn Asp His His Trp His Glu Gly Asn
            185                 190                 195

tac tac gaa tcc ggc tgc aac cca gcc acc gga ctc ggc gcc gcc cga    739
Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly Leu Gly Ala Ala Arg
        200                 205                 210

cgc atc gcc cac ctc acc tac cgt ggc gaa cta gaa atc gac gaa cgc    787
Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu Glu Ile Asp Glu Arg
    215                 220                 225

ttc ggc acc aaa gcc caa aag aac gaa aac cca ctc ggt ccc tac cgc    835
Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro Leu Gly Pro Tyr Arg
230                 235                 240                 245

aag ccc gac cag cgc ttc gcc gtg gaa tcc tac ttg gac tac caa gca    883
Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr Leu Asp Tyr Gln Ala
                250                 255                 260

gac aag cta gta cag cgt ttc gac gcc ggc tcc tac gtc ttg ctc acc    931
Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser Tyr Val Leu Leu Thr
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265 270 275

gac gcc ctc aac cgc cac gac att ggt cgc gac cgc gga ggc ctc aac 979
Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp Arg Gly Gly Leu Asn
280 285 290

aag gca ctc gaa tcc atc aaa gtt cca gtc ctt gtc gca ggc gta gat 1027
Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu Val Ala Gly Val Asp
295 300 305

acc gat att ttg tac ccc tac cac cag caa gaa cac ctc tcc aga aac 1075
Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu His Leu Ser Arg Asn
310 315 320 325

ctg gga aat cta ctg gca atg gca aaa atc gta tcc cct gtc ggc cac 1123
Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val Ser Pro Val Gly His
330 335 340

gat gct ttc ctc acc gaa agc cgc caa atg gat cgc atc gtg agg aac 1171
Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp Arg Ile Val Arg Asn
345 350 355

ttc ttc agc ctc atc tcc cca gac gaa gac aac cct tcg 1210
Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn Pro Ser
360 365 370

<210> 74
<211> 370
<212> PRT
<213> Corynebacterium glutamicum

<400> 74
Met Pro Thr Leu Ala Pro Ser Gly Gln Leu Glu Ile Gln Ala Ile Gly
1 5 10 15

Asp Val Ser Thr Glu Ala Gly Ala Ile Ile Thr Asn Ala Glu Ile Ala
20 25 30

Tyr His Arg Trp Gly Glu Tyr Arg Val Asp Lys Glu Gly Arg Ser Asn
35 40 45

Val Val Leu Ile Glu His Ala Leu Thr Gly Asp Ser Asn Ala Ala Asp
50 55 60

Trp Trp Ala Asp Leu Leu Gly Pro Gly Lys Ala Ile Asn Thr Asp Ile
65 70 75 80

Tyr Cys Val Ile Cys Thr Asn Val Ile Gly Gly Cys Asn Gly Ser Thr
85 90 95

Gly Pro Gly Ser Met His Pro Asp Gly Asn Phe Trp Gly Asn Arg Phe
100 105 110

Pro Ala Thr Ser Ile Arg Asp Gln Val Asn Ala Glu Lys Gln Phe Leu
115 120 125

Asp Ala Leu Gly Ile Thr Thr Val Ala Ala Val Leu Gly Gly Ser Met
130 135 140

Gly Gly Ala Arg Thr Leu Glu Trp Ala Ala Met Tyr Pro Glu Thr Val

145 150 155 160

Gly Ala Ala Ala Val Leu Ala Val Ser Ala Arg Ala Ser Ala Trp Gln
165 170 175

Ile Gly Ile Gln Ser Ala Gln Ile Lys Ala Ile Glu Asn Asp His His
180 185 190

Trp His Glu Gly Asn Tyr Tyr Glu Ser Gly Cys Asn Pro Ala Thr Gly
195 200 205

Leu Gly Ala Ala Arg Arg Ile Ala His Leu Thr Tyr Arg Gly Glu Leu
210 215 220

Glu Ile Asp Glu Arg Phe Gly Thr Lys Ala Gln Lys Asn Glu Asn Pro
225 230 235 240

Leu Gly Pro Tyr Arg Lys Pro Asp Gln Arg Phe Ala Val Glu Ser Tyr
245 250 255

Leu Asp Tyr Gln Ala Asp Lys Leu Val Gln Arg Phe Asp Ala Gly Ser
260 265 270

Tyr Val Leu Leu Thr Asp Ala Leu Asn Arg His Asp Ile Gly Arg Asp
275 280 285

Arg Gly Gly Leu Asn Lys Ala Leu Glu Ser Ile Lys Val Pro Val Leu
290 295 300

Val Ala Gly Val Asp Thr Asp Ile Leu Tyr Pro Tyr His Gln Gln Glu
305 310 315 320

His Leu Ser Arg Asn Leu Gly Asn Leu Leu Ala Met Ala Lys Ile Val
325 330 335

Ser Pro Val Gly His Asp Ala Phe Leu Thr Glu Ser Arg Gln Met Asp
340 345 350

Arg Ile Val Arg Asn Phe Phe Ser Leu Ile Ser Pro Asp Glu Asp Asn
355 360 365

Pro Ser
370

<210> 75
<211> 687
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(664)
<223> RXS03158

<400> 75
caaagctcac cgaaggcacc aacgccaagt tggttgttga caacaccttg gcatccccat 60

acctgcagca gccactaaaa ctcggcgcac acgcaagtcc ttg cac tcc acc acc 115
Leu His Ser Thr Thr
1 5

aag tac atc gaa gga cac tcc gac gtt gtt ggc ggc ctt gtg ggt acc 163
Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly Gly Leu Val Gly Thr
10 15 20

aac gac cag gaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc 211
Asn Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile
25 30 35

gga ccg atc cca tca gtt ttc gat gca tac ctg acc gcc cgt ggc ctc 259
Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu
40 45 50

aag acc ctt gca gtg cgc atg gat cgc cac tgc gac aac gca gaa aag 307
Lys Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys
55 60 65

atc gcg gaa ttc ctg gac tcc cgc cca gag gtc tcc acc gtg ctc tac 355
Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr
70 75 80 85

cca ggt ctg aag aac cac cca ggc cac gaa gtc gca gcg aag cag atg 403
Pro Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met
90 95 100

aag cgc ttc ggc ggc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa 451
Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu
105 110 115

gca gct aag aag ttc tgt acc tcc acc aaa ctg atc tgt ctg gcc gag 499
Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu
120 125 130

tcc ctc ggt ggc gtg gaa tcc ctc ctg gag cac cca gca acc atg acc 547
Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr
135 140 145

cac cag tca gct gcc ggc tct cag ctc gag gtt ccc cgc gac ctc gtg 595
His Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val
150 155 160 165

cgc atc tcc att ggt att gaa gac att gaa gac ctg ctc gca gat gtc 643
Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val
170 175 180

gag cag gcc ctc aat aac ctt tagaaactat ttggcggcaa gca 687
Glu Gln Ala Leu Asn Asn Leu
185

<210> 76
<211> 188
<212> PRT
<213> Corynebacterium glutamicum

<400> 76
Leu His Ser Thr Thr Lys Tyr Ile Glu Gly His Ser Asp Val Val Gly
1 5 10 15

Gly Leu Val Gly Thr Asn Asp Gln Glu Met Asp Glu Glu Leu Leu Phe
20 25 30

Met Gln Gly Gly Ile Gly Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu
35 40 45

Thr Ala Arg Gly Leu Lys Thr Leu Ala Val Arg Met Asp Arg His Cys
50 55 60

Asp Asn Ala Glu Lys Ile Ala Glu Phe Leu Asp Ser Arg Pro Glu Val
65 70 75 80

Ser Thr Val Leu Tyr Pro Gly Leu Lys Asn His Pro Gly His Glu Val
85 90 95

Ala Ala Lys Gln Met Lys Arg Phe Gly Gly Met Ile Ser Val Arg Phe
100 105 110

Ala Gly Gly Glu Glu Ala Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu
115 120 125

Ile Cys Leu Ala Glu Ser Leu Gly Gly Val Glu Ser Leu Leu Glu His
130 135 140

Pro Ala Thr Met Thr His Gln Ser Ala Ala Gly Ser Gln Leu Glu Val
145 150 155 160

Pro Arg Asp Leu Val Arg Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp
165 170 175

Leu Leu Ala Asp Val Glu Gln Ala Leu Asn Asn Leu
180 185

<210> 77
<211> 617
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(594)
<223> FRXA00254

<400> 77
cag cca cta aaa ctc ggc gca cac gca gtc ttg cac tcc acc acc aag 48
Gln Pro Leu Lys Leu Gly Ala His Ala Val Leu His Ser Thr Thr Lys
1 5 10 15

tac atc gga gga cac tcc gac gtt gtt ggc ggc ctt gtg gtt acc aac 96
Tyr Ile Gly Gly His Ser Asp Val Val Gly Gly Leu Val Val Thr Asn
20 25 30

gac cag gaa atg gac gaa gaa ctg ctg ttc atg cag ggc ggc atc gga 144
Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile Gly
35 40 45

ccg atc cca tca gtt ttc gat gca tac ctg acc gcc cgt ggc ctc aag 192
Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys
50 55 60

acc ctt gca gtg cgc atg gat cgc cac tgc gac aac gca gaa aag atc 240
Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile

65 70 75 80

gcg gaa ttc ctg gac tcc cgc cca gag gtc tcc acc gtg ctc tac cca 288
Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro
85 90 95

ggt ctg aag aac cac cca ggc cac gaa gtc gca gcg aag cag atg aag 336
Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys
100 105 110

cgc ttc ggc ggc atg atc tcc gtc cgt ttc gca ggc ggc gaa gaa gca 384
Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala
115 120 125

gct aag aag ttc tgt acc tcc acc aaa ctg atc tgt ctg gcc gag tcc 432
Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser
130 135 140

ctc ggt ggc gtg gaa tcc ctc ctg gag cac cca gca acc atg acc cac 480
Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr His
145 150 155 160

cag tca gct gcc ggc tct cag ctc gag gtt ccc cgc gac ctc gtg cgc 528
Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg
165 170 175

atc tcc att ggt att gaa gac att gaa gac ctg ctc gca gat gtc gag 576
Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Glu
180 185 190

cag gcc ctc aat aac ctt tagaaactat ttggcggcaa gca 617
Gln Ala Leu Asn Asn Leu
195

<210> 78
<211> 198
<212> PRT
<213> Corynebacterium glutamicum

<400> 78
Gln Pro Leu Lys Leu Gly Ala His Ala Val Leu His Ser Thr Thr Lys
1 5 10 15

Tyr Ile Gly Gly His Ser Asp Val Val Gly Gly Leu Val Val Thr Asn
20 25 30

Asp Gln Glu Met Asp Glu Glu Leu Leu Phe Met Gln Gly Gly Ile Gly
35 40 45

Pro Ile Pro Ser Val Phe Asp Ala Tyr Leu Thr Ala Arg Gly Leu Lys
50 55 60

Thr Leu Ala Val Arg Met Asp Arg His Cys Asp Asn Ala Glu Lys Ile
65 70 75 80

Ala Glu Phe Leu Asp Ser Arg Pro Glu Val Ser Thr Val Leu Tyr Pro
85 90 95

Gly Leu Lys Asn His Pro Gly His Glu Val Ala Ala Lys Gln Met Lys
100 105 110

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Arg Phe Gly Gly Met Ile Ser Val Arg Phe Ala Gly Gly Glu Glu Ala
        115                 120                 125

Ala Lys Lys Phe Cys Thr Ser Thr Lys Leu Ile Cys Leu Ala Glu Ser
    130                 135                 140

Leu Gly Gly Val Glu Ser Leu Leu Glu His Pro Ala Thr Met Thr His
145                 150                 155                 160

Gln Ser Ala Ala Gly Ser Gln Leu Glu Val Pro Arg Asp Leu Val Arg
                165                 170                 175

Ile Ser Ile Gly Ile Glu Asp Ile Glu Asp Leu Leu Ala Asp Val Glu
            180                 185                 190

Gln Ala Leu Asn Asn Leu
        195


<210> 79
<211> 1170
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1147)
<223> RXA02532

<400> 79
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tgtgcaagcg ggacggccag ccagaactcc tggtgcgccg atg aac cca cct atc   115
                                            Met Asn Pro Pro Ile
                                             1               5

acg ttg tcc agc act tat gtt cat gat tca gaa aaa gct tat ggg cgc   163
Thr Leu Ser Ser Thr Tyr Val His Asp Ser Glu Lys Ala Tyr Gly Arg
                10                  15                  20

gat ggc aat gat gga tgg ggt gca ttt gag gct gcc atg gga act cta   211
Asp Gly Asn Asp Gly Trp Gly Ala Phe Glu Ala Ala Met Gly Thr Leu
            25                  30                  35

gat ggt ggg ttc gcg gta tct tat tct tca ggt ttg gca gcg gca acg   259
Asp Gly Gly Phe Ala Val Ser Tyr Ser Ser Gly Leu Ala Ala Ala Thr
        40                  45                  50

tcg att gct gat ttg gtt cct act ggt ggc aca gtt gtt tta cct aaa   307
Ser Ile Ala Asp Leu Val Pro Thr Gly Gly Thr Val Val Leu Pro Lys
    55                  60                  65

gct gcc tat tat ggc gtg acc aat att ttc gcc agg atg gaa gcc cgc   355
Ala Ala Tyr Tyr Gly Val Thr Asn Ile Phe Ala Arg Met Glu Ala Arg
 70                  75                  80                  85

gga agg ctg aag gtt cga act gtt gat gca gac aat acc gaa gaa gtg   403
Gly Arg Leu Lys Val Arg Thr Val Asp Ala Asp Asn Thr Glu Glu Val
                90                  95                  100
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att gct gct gct caa ggt gca gat gtg gtg tgg gtg gaa tcg atc gct    451
Ile Ala Ala Ala Gln Gly Ala Asp Val Val Trp Val Glu Ser Ile Ala
            105                 110                 115

aat ccg acg atg gtg gta gct gat atc cct gca ata gtc gac ggt gtg    499
Asn Pro Thr Met Val Val Ala Asp Ile Pro Ala Ile Val Asp Gly Val
        120                 125                 130

cgt ggg ctt gga gtt ttg act gtc gtt gac gcg act ttc gca acg cca    547
Arg Gly Leu Gly Val Leu Thr Val Val Asp Ala Thr Phe Ala Thr Pro
    135                 140                 145

ctt cgt caa cgt cca ttg gaa ctt ggt gct gat att gtg ctt tac tcg    595
Leu Arg Gln Arg Pro Leu Glu Leu Gly Ala Asp Ile Val Leu Tyr Ser
150                 155                 160                 165

gca acc aaa ctt atc ggt gga cac tct gat ctt ctt ctt gga gtc gca    643
Ala Thr Lys Leu Ile Gly Gly His Ser Asp Leu Leu Leu Gly Val Ala
                170                 175                 180

gtg tgc aag tct gag cac cat gcg cag ttt ctt gcc act cac cgt cat    691
Val Cys Lys Ser Glu His His Ala Gln Phe Leu Ala Thr His Arg His
            185                 190                 195

gat cat ggt tca gtg ccg gga ggt ctt gaa gcg ttt ctt gct ctc cgt    739
Asp His Gly Ser Val Pro Gly Gly Leu Glu Ala Phe Leu Ala Leu Arg
        200                 205                 210

gga ttg tat tcc ttg gcg gtg cgt ctt gat cga gca gaa tcc aac gca    787
Gly Leu Tyr Ser Leu Ala Val Arg Leu Asp Arg Ala Glu Ser Asn Ala
    215                 220                 225

gca gaa ctt tcg cgg cga ctt aac gcg cat cct tcg gtt acc cgc gtc    835
Ala Glu Leu Ser Arg Arg Leu Asn Ala His Pro Ser Val Thr Arg Val
230                 235                 240                 245

aat tat cca gga ctt cct gat gat ccc caa cat gaa aaa gcc gtg cga    883
Asn Tyr Pro Gly Leu Pro Asp Asp Pro Gln His Glu Lys Ala Val Arg
                250                 255                 260

gtc cta ccc tct gga tgt gga aac atg ttg tca ttt gag ctt gat gca    931
Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser Phe Glu Leu Asp Ala
            265                 270                 275

aca cct gaa cga act gat gag att ctc gaa agc ctg tca ctt tta acc    979
Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser Leu Ser Leu Leu Thr
        280                 285                 290

cac gcg acc agt tgg gga ggt gtg gaa aca gcc att gaa cgt cgc acc    1027
His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala Ile Glu Arg Arg Thr
    295                 300                 305

agg cgg gat gct gaa gtg gtg gca gaa gta ccg atg act ctt tgc cgc    1075
Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro Met Thr Leu Cys Arg
310                 315                 320                 325

gtt tcc gta gga att gaa gac gtt gaa gat cta tgg gaa gac ctc aac    1123
Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu Trp Glu Asp Leu Asn
                330                 335                 340

gcc tca atc gac aaa gtt ctg ggt tagaactcgt agccagtaac cag          1170
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Ala Ser Ile Asp Lys Val Leu Gly
345

<210> 80
<211> 349
<212> PRT
<213> Corynebacterium glutamicum

<400> 80
Met Asn Pro Pro Ile Thr Leu Ser Ser Thr Tyr Val His Asp Ser Glu
1 5 10 15

Lys Ala Tyr Gly Arg Asp Gly Asn Asp Gly Trp Gly Ala Phe Glu Ala
20 25 30

Ala Met Gly Thr Leu Asp Gly Gly Phe Ala Val Ser Tyr Ser Ser Gly
35 40 45

Leu Ala Ala Ala Thr Ser Ile Ala Asp Leu Val Pro Thr Gly Gly Thr
50 55 60

Val Val Leu Pro Lys Ala Ala Tyr Tyr Gly Val Thr Asn Ile Phe Ala
65 70 75 80

Arg Met Glu Ala Arg Gly Arg Leu Lys Val Arg Thr Val Asp Ala Asp
85 90 95

Asn Thr Glu Glu Val Ile Ala Ala Ala Gln Gly Ala Asp Val Val Trp
100 105 110

Val Glu Ser Ile Ala Asn Pro Thr Met Val Val Ala Asp Ile Pro Ala
115 120 125

Ile Val Asp Gly Val Arg Gly Leu Gly Val Leu Thr Val Val Asp Ala
130 135 140

Thr Phe Ala Thr Pro Leu Arg Gln Arg Pro Leu Glu Leu Gly Ala Asp
145 150 155 160

Ile Val Leu Tyr Ser Ala Thr Lys Leu Ile Gly Gly His Ser Asp Leu
165 170 175

Leu Leu Gly Val Ala Val Cys Lys Ser Glu His His Ala Gln Phe Leu
180 185 190

Ala Thr His Arg His Asp His Gly Ser Val Pro Gly Gly Leu Glu Ala
195 200 205

Phe Leu Ala Leu Arg Gly Leu Tyr Ser Leu Ala Val Arg Leu Asp Arg
210 215 220

Ala Glu Ser Asn Ala Ala Glu Leu Ser Arg Arg Leu Asn Ala His Pro
225 230 235 240

Ser Val Thr Arg Val Asn Tyr Pro Gly Leu Pro Asp Asp Pro Gln His
245 250 255

Glu Lys Ala Val Arg Val Leu Pro Ser Gly Cys Gly Asn Met Leu Ser
260 265 270

```
Phe Glu Leu Asp Ala Thr Pro Glu Arg Thr Asp Glu Ile Leu Glu Ser
        275                 280                 285

Leu Ser Leu Leu Thr His Ala Thr Ser Trp Gly Gly Val Glu Thr Ala
    290                 295                 300

Ile Glu Arg Arg Thr Arg Arg Asp Ala Glu Val Val Ala Glu Val Pro
305                 310                 315                 320

Met Thr Leu Cys Arg Val Ser Val Gly Ile Glu Asp Val Glu Asp Leu
                325                 330                 335

Trp Glu Asp Leu Asn Ala Ser Ile Asp Lys Val Leu Gly
            340                 345


<210> 81
<211> 861
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(838)
<223> RXS03159

<400> 81
aggggctagt tttacacaaa agtggacagc ttggtctatc attgccagaa gaccggtcct 60

tttagggcca tagaattctg attacaggag ttgatctacc ttg tct ttt gac cca   115
                                              Leu Ser Phe Asp Pro
                                                1               5

aac acc cag ggt ttc tcc act gca tcg att cac gct ggg tat gag cca   163
Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His Ala Gly Tyr Glu Pro
                10                  15                  20

gac gac tac tac ggt tcg att aac acc cca atc tat gcc tcc acc acc   211
Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr
            25                  30                  35

ttc gcg cag aac gct cca aac gaa ctg cgc aaa ggc tac gag tac acc   259
Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr
        40                  45                  50

cgt gtg ggc aac ccc acc atc gtg gca tta gag cag acc gtc gca gca   307
Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Gln Thr Val Ala Ala
    55                  60                  65

ctc gaa ggc gca aag tat ggc cgc gca ttc tcc tcc ggc atg gct gca   355
Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala
70                  75                  80                  85

acc gac atc ctg ttc cgc atc atc ctc aag ccg ggc gat cac atc gtc   403
Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val
                90                  95                  100

ctc ggc aac gat gct tac ggc gga acc tac cgc ctg atc gac acc gta   451
Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val
            105                 110                 115
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ttc acc gca tgg ggc gtc gaa tac acc gtt gtt gat acc tcc gtc gtg 499
Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val Asp Thr Ser Val Val
120 125 130

gaa gag gtc aag gca gcg atc aag gac aac acc aag ctg atc tgg gtg 547
Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr Lys Leu Ile Trp Val
135 140 145

gaa acc cca acc aac cca gca ctt ggc atc acc gac atc gaa gca gta 595
Glu Thr Pro Thr Asn Pro Ala Leu Gly Ile Thr Asp Ile Glu Ala Val
150 155 160 165

gca aag ctc acc gaa ggc acc aac gcc aag ttg gtt gtt gac aac acc 643
Ala Lys Leu Thr Glu Gly Thr Asn Ala Lys Leu Val Val Asp Asn Thr
170 175 180

ttg gca tcc cca tac ctg cag cag cca cta aaa ctc ggc gca cac gca 691
Leu Ala Ser Pro Tyr Leu Gln Gln Pro Leu Lys Leu Gly Ala His Ala
185 190 195

agt cct tgc act cca cca cca agt aca tcg aag gac act ccg acg ttg 739
Ser Pro Cys Thr Pro Pro Pro Ser Thr Ser Lys Asp Thr Pro Thr Leu
200 205 210

ttg gcg gcc ttg tgg gta cca acg acc agg aaa tgg acg aag aac tgc 787
Leu Ala Ala Leu Trp Val Pro Thr Thr Arg Lys Trp Thr Lys Asn Cys
215 220 225

tgt tca tgc agg gcg gca tcg gac cga tcc cat cag ttt tcg atg cat 835
Cys Ser Cys Arg Ala Ala Ser Asp Arg Ser His Gln Phe Ser Met His
230 235 240 245

acc tgaccgcccg tggcctcaag acc 861
Thr

<210> 82
<211> 246
<212> PRT
<213> Corynebacterium glutamicum

<400> 82
Leu Ser Phe Asp Pro Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His
1 5 10 15

Ala Gly Tyr Glu Pro Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile
20 25 30

Tyr Ala Ser Thr Thr Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys
35 40 45

Gly Tyr Glu Tyr Thr Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu
50 55 60

Gln Thr Val Ala Ala Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser
65 70 75 80

Ser Gly Met Ala Ala Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro
85 90 95

Gly Asp His Ile Val Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg
100 105 110

Leu Ile Asp Thr Val Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val
115 120 125

Asp Thr Ser Val Val Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr
130 135 140

Lys Leu Ile Trp Val Glu Thr Pro Thr Asn Pro Ala Leu Gly Ile Thr
145 150 155 160

Asp Ile Glu Ala Val Ala Lys Leu Thr Glu Gly Thr Asn Ala Lys Leu
165 170 175

Val Val Asp Asn Thr Leu Ala Ser Pro Tyr Leu Gln Gln Pro Leu Lys
180 185 190

Leu Gly Ala His Ala Ser Pro Cys Thr Pro Pro Pro Ser Thr Ser Lys
195 200 205

Asp Thr Pro Thr Leu Leu Ala Ala Leu Trp Val Pro Thr Thr Arg Lys
210 215 220

Trp Thr Lys Asn Cys Cys Ser Cys Arg Ala Ala Ser Asp Arg Ser His
225 230 235 240

Gln Phe Ser Met His Thr
245

<210> 83
<211> 703
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(703)
<223> FRXA02768

<220>
<223> All occurrences of n = any nucleotide

<220>
<223> All occurrences of Xaa = any amino acid

<400> 83
aggggctagt tttacacaaa agtggacagc ttggtctatc attgccagaa gaccggtcct 60

tttagggcca tagaattctg attacaggag ttgatctacc ttg tct ttt gac cca 115
Leu Ser Phe Asp Pro
1 5

aac acc cag ggt ttc tcc act gca tcg att cac gct ggg tat gag cca 163
Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His Ala Gly Tyr Glu Pro
10 15 20

gac gac tac tac ggt tcg att aac acc cca atc tat gcc tcc acc acc 211
Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile Tyr Ala Ser Thr Thr
25 30 35

```
ttc gcg cag aac gct cca aac gaa ctg cgc aaa ggc tac gag tac acc   259
Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys Gly Tyr Glu Tyr Thr
         40                  45                  50

cgt gtg ggc aac ccc acc atc gtg gca tta gag cag acc gtc gca gca   307
Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu Gln Thr Val Ala Ala
     55                  60                  65

ctc gaa ggc gca aag tat ggc cgc gca ttc tcc tcc ggc atg gct gca   355
Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser Ser Gly Met Ala Ala
 70                  75                  80                  85

acc gac atc ctg ttc cgc atc atc ctc aag ccg ggc gat cac atc gtc   403
Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro Gly Asp His Ile Val
                 90                  95                 100

ctc ggc aac gat gct tac ggc gga acc tac cgc ctg atc gac acc gta   451
Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg Leu Ile Asp Thr Val
            105                 110                 115

ttc acc gca tgg ggc gtc gaa tac acc gtt gtt gat acc tcc gtc gtg   499
Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val Asp Thr Ser Val Val
        120                 125                 130

gaa gag gtc aag gca gcg atc aag gac aac acc aag gct gat ctt ggt   547
Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr Lys Ala Asp Leu Gly
    135                 140                 145

gga aac ccc aac caa ccc agc act ttg gca tta ccc gac atc gaa gca   595
Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu Pro Asp Ile Glu Ala
150                 155                 160                 165

gtn tgc aaa act tca ccc gaa agg cac caa ccc caa gct tgt tgt ttg   643
Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro Gln Ala Cys Cys Leu
                170                 175                 180

aca aca cct tcg cat tcc cca tac ctg cag can cca ctt aaa ant tnn   691
Thr Thr Pro Ser His Ser Pro Tyr Leu Gln Xaa Pro Leu Lys Xaa Xaa
            185                 190                 195

gng cac acg cag                                                  703
Xaa His Thr Gln
        200
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<210> 84
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

<220>
<223> All occurrences of Xaa = any amino acid

<400> 84

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Leu Ser Phe Asp Pro Asn Thr Gln Gly Phe Ser Thr Ala Ser Ile His
  1               5                  10                  15

Ala Gly Tyr Glu Pro Asp Asp Tyr Tyr Gly Ser Ile Asn Thr Pro Ile
             20                  25                  30
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```
Tyr Ala Ser Thr Thr Phe Ala Gln Asn Ala Pro Asn Glu Leu Arg Lys
         35                  40                  45

Gly Tyr Glu Tyr Thr Arg Val Gly Asn Pro Thr Ile Val Ala Leu Glu
     50                  55                  60

Gln Thr Val Ala Ala Leu Glu Gly Ala Lys Tyr Gly Arg Ala Phe Ser
 65                  70                  75                  80

Ser Gly Met Ala Ala Thr Asp Ile Leu Phe Arg Ile Ile Leu Lys Pro
                 85                  90                  95

Gly Asp His Ile Val Leu Gly Asn Asp Ala Tyr Gly Gly Thr Tyr Arg
            100                 105                 110

Leu Ile Asp Thr Val Phe Thr Ala Trp Gly Val Glu Tyr Thr Val Val
        115                 120                 125

Asp Thr Ser Val Val Glu Glu Val Lys Ala Ala Ile Lys Asp Asn Thr
    130                 135                 140

Lys Ala Asp Leu Gly Gly Asn Pro Asn Gln Pro Ser Thr Leu Ala Leu
145                 150                 155                 160

Pro Asp Ile Glu Ala Val Cys Lys Thr Ser Pro Glu Arg His Gln Pro
                165                 170                 175

Gln Ala Cys Cys Leu Thr Thr Pro Ser His Ser Pro Tyr Leu Gln Xaa
            180                 185                 190

Pro Leu Lys Xaa Xaa Xaa His Thr Gln
        195                 200
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<210> 85
<211> 1113
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1090)
<223> RXA00216

<400> 85
gtgttgctcg cggccaggca gcagtgctgt acctgcctga cgcggatggt gacatcgttc 60

ttggatcagg caccatctgc cacacggagt cttaagaaaa ttg ggc gct tat ggt 115
                                              Leu Gly Ala Tyr Gly
                                                1   5

tta ggt gag ctt cct gga aaa tcc gcc gcg gaa gcc gcc gac att att 163
Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu Ala Ala Asp Ile Ile
                 10   15   20

cag ggt gaa acg ggc gat ctt ctc cat att cct cag ctt ccg gcg cga 211
Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro Gln Leu Pro Ala Arg
             25   30   35

ggt ttg ggt gct gat ctg atc ggt cga acc gtc ggt ctg ctg gac atg 259
Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val Gly Leu Leu Asp Met
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```

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        40                  45                  50

atc aac gtt gat cgc ggg gcc cga tct tgg gtg atg agc aca cgc ccc     307
Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val Met Ser Thr Arg Pro
    55                  60                  65

agc aga ttg acg cac ctg acc ggc gat ttc ctt gac atg gat ttg gat     355
Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu Asp Met Asp Leu Asp
 70                  75                  80                  85

gcg tgc gag gaa acc tgg gga acg ggc gtc gac aag cta aaa atc caa     403
Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp Lys Leu Lys Ile Gln
                 90                  95                 100

gtt gct ggt ccc tgg act tta ggt gcg cgc att gag ttg gcc aat ggc     451
Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile Glu Leu Ala Asn Gly
            105                 110                 115

cat cgc gtt ttg tct gat cgc ggt gcg atg cgt gat ctc acg cag gcg     499
His Arg Val Leu Ser Asp Arg Gly Ala Met Arg Asp Leu Thr Gln Ala
        120                 125                 130

ctg atc gcc ggc atc gat gcg cat gca cgc aag gtt gct ggg cga ttt     547
Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys Val Ala Gly Arg Phe
    135                 140                 145

cgc gcc gaa gtg cag gtg caa att gat gag ccg gag ctg aaa tcg ctt     595
Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro Glu Leu Lys Ser Leu
150                 155                 160                 165

atc gac ggc tcc ctc cct ggc act tcc acc ttt gac att att cct gcg     643
Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe Asp Ile Ile Pro Ala
                170                 175                 180

gtg aat gtc gct gat gcc agt gaa cgt ttg cag cag gtc ttt agc tcg     691
Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln Gln Val Phe Ser Ser
            185                 190                 195

att gag ggg ccg aca tat ctc aac ctc acc ggc cag att cct act tgg     739
Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly Gln Ile Pro Thr Trp
        200                 205                 210

gat gtg gct cgg ggt gcg ggc gcc gat act gtg cag att tcc atg gat     787
Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val Gln Ile Ser Met Asp
    215                 220                 225

caa gtc cgt gga aat gaa cat ttg gat ggt ttt ggt gaa acc atc acc     835
Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe Gly Glu Thr Ile Thr
230                 235                 240                 245

agt gga att cgt ctt ggt ttg ggc att acg aca gga aaa gat gtc gta     883
Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr Gly Lys Asp Val Val
                250                 255                 260

gat gaa ctg ctc gag cga ccg cgg caa aag gcc gtt gag gta gca cgc     931
Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala Val Glu Val Ala Arg
            265                 270                 275

ttt ttt gat cgt tta ggt gtg ggc cga aac tat ctc gtg gat gct gtt     979
Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr Leu Val Asp Ala Val
        280                 285                 290
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```
gat att cat ccg ggt gag gat ttg gtg cag ggg acc atc acc gag gcc     1027
Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly Thr Ile Thr Glu Ala
    295                 300                 305

gcg cag gct tat cgc atg gcc cgg gtg atg tcg gag atg ttg tcg aag     1075
Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser Glu Met Leu Ser Lys
310                 315                 320                 325

gat tca tgc gac ctt taaggcttta ccggcgctgg gtg                       1113
Asp Ser Cys Asp Leu
                330


<210> 86
<211> 330
<212> PRT
<213> Corynebacterium glutamicum

<400> 86
Leu Gly Ala Tyr Gly Leu Gly Glu Leu Pro Gly Lys Ser Ala Ala Glu
  1               5                  10                  15

Ala Ala Asp Ile Ile Gln Gly Glu Thr Gly Asp Leu Leu His Ile Pro
             20                  25                  30

Gln Leu Pro Ala Arg Gly Leu Gly Ala Asp Leu Ile Gly Arg Thr Val
         35                  40                  45

Gly Leu Leu Asp Met Ile Asn Val Asp Arg Gly Ala Arg Ser Trp Val
     50                  55                  60

Met Ser Thr Arg Pro Ser Arg Leu Thr His Leu Thr Gly Asp Phe Leu
 65                  70                  75                  80

Asp Met Asp Leu Asp Ala Cys Glu Glu Thr Trp Gly Thr Gly Val Asp
                 85                  90                  95

Lys Leu Lys Ile Gln Val Ala Gly Pro Trp Thr Leu Gly Ala Arg Ile
            100                 105                 110

Glu Leu Ala Asn Gly His Arg Val Leu Ser Asp Arg Gly Ala Met Arg
        115                 120                 125

Asp Leu Thr Gln Ala Leu Ile Ala Gly Ile Asp Ala His Ala Arg Lys
    130                 135                 140

Val Ala Gly Arg Phe Arg Ala Glu Val Gln Val Gln Ile Asp Glu Pro
145                 150                 155                 160

Glu Leu Lys Ser Leu Ile Asp Gly Ser Leu Pro Gly Thr Ser Thr Phe
                165                 170                 175

Asp Ile Ile Pro Ala Val Asn Val Ala Asp Ala Ser Glu Arg Leu Gln
            180                 185                 190

Gln Val Phe Ser Ser Ile Glu Gly Pro Thr Tyr Leu Asn Leu Thr Gly
        195                 200                 205

Gln Ile Pro Thr Trp Asp Val Ala Arg Gly Ala Gly Ala Asp Thr Val
    210                 215                 220
```

Gln Ile Ser Met Asp Gln Val Arg Gly Asn Glu His Leu Asp Gly Phe
225 230 235 240

Gly Glu Thr Ile Thr Ser Gly Ile Arg Leu Gly Leu Gly Ile Thr Thr
245 250 255

Gly Lys Asp Val Val Asp Glu Leu Leu Glu Arg Pro Arg Gln Lys Ala
260 265 270

Val Glu Val Ala Arg Phe Phe Asp Arg Leu Gly Val Gly Arg Asn Tyr
275 280 285

Leu Val Asp Ala Val Asp Ile His Pro Gly Glu Asp Leu Val Gln Gly
290 295 300

Thr Ile Thr Glu Ala Ala Gln Ala Tyr Arg Met Ala Arg Val Met Ser
305 310 315 320

Glu Met Leu Ser Lys Asp Ser Cys Asp Leu
325 330

<210> 87
<211> 551
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(528)
<223> RXA02197

<400> 87
gcc gaa cgc atg cgc ttt agc ttc cca cgc cag cag cgc ggc agg ttc 48
Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe
1 5 10 15

ttg tgc atc gcg gat ttc att cgc cca cgc gag caa gct gtc aag gac 96
Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp
20 25 30

ggc caa gtg gac gtc atg cca ttc cag ctg gtc acc atg ggt aat cct 144
Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro
35 40 45

att gct gat ttc gcc aac gag ttg ttc gca gcc aat gaa tac cgc gag 192
Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
50 55 60

tac ttg gaa gtt cac ggc atc ggc gtg cag ctc acc gaa gca ttg gcc 240
Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
65 70 75 80

gag tac tgg cac tcc cga gtg cgc agc gaa ctc aag ctg aac gac ggt 288
Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
85 90 95

gga tct gtc gct gat ttt gat cca gaa gac aag acc aag ttc ttc gac 336
Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
100 105 110

```
ctg gat tac cgc ggc gcc cgc ttc tcc ttt ggt tac ggt tct tgc cct   384
Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
        115                 120                 125

gat ctg gaa gac cgc gca aag ctg gtg gaa ttg ctc gag cca ggc cgt   432
Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg
    130                 135                 140

atc ggc gtg gag ttg tcc gag gaa ctc cag ctg cac cca gag cag tcc   480
Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
145                 150                 155                 160

aca gac gcg ttt gtg ctc tac cac cca gag gca aag tac ttt aac gtc   528
Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
                165                 170                 175

taacaccttt gagagggaaa act                                       551
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<210> 88
<211> 176
<212> PRT
<213> Corynebacterium glutamicum

<400> 88

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Ala Glu Arg Met Arg Phe Ser Phe Pro Arg Gln Gln Arg Gly Arg Phe
  1               5                  10                  15

Leu Cys Ile Ala Asp Phe Ile Arg Pro Arg Glu Gln Ala Val Lys Asp
             20                  25                  30

Gly Gln Val Asp Val Met Pro Phe Gln Leu Val Thr Met Gly Asn Pro
         35                  40                  45

Ile Ala Asp Phe Ala Asn Glu Leu Phe Ala Ala Asn Glu Tyr Arg Glu
     50                  55                  60

Tyr Leu Glu Val His Gly Ile Gly Val Gln Leu Thr Glu Ala Leu Ala
 65                  70                  75                  80

Glu Tyr Trp His Ser Arg Val Arg Ser Glu Leu Lys Leu Asn Asp Gly
                 85                  90                  95

Gly Ser Val Ala Asp Phe Asp Pro Glu Asp Lys Thr Lys Phe Phe Asp
            100                 105                 110

Leu Asp Tyr Arg Gly Ala Arg Phe Ser Phe Gly Tyr Gly Ser Cys Pro
        115                 120                 125

Asp Leu Glu Asp Arg Ala Lys Leu Val Glu Leu Leu Glu Pro Gly Arg
    130                 135                 140

Ile Gly Val Glu Leu Ser Glu Glu Leu Gln Leu His Pro Glu Gln Ser
145                 150                 155                 160

Thr Asp Ala Phe Val Leu Tyr His Pro Glu Ala Lys Tyr Phe Asn Val
                165                 170                 175
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<210> 89

<211> 2599
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2599)
<223> RXN02198

<400> 89
agactagtgg cgctttgcct gtgttgctta ggcggcgttg aaaatgaact acgaatgaaa 60

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agttcgggaa ttgtctaatc cgtactaagc tgtctacaca atg tct act tca gtt   115
                                            Met Ser Thr Ser Val
                                              1               5

act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg   163
Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala
                 10                  15                  20

ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc   211
Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu
             25                  30                  35

caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg   259
Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly
         40                  45                  50

tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att   307
Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile
     55                  60                  65

cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act   355
His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr
 70                  75                  80                  85

ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt   403
Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg
                 90                  95                 100

tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct   451
Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala
             105                 110                 115

gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt   499
Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly
         120                 125                 130

tcc ctg gga cct gga acg aag ctt cca tcg ctg ggc cat gca ccg tat   547
Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr
    135                 140                 145

gca gat ttg cgt ggg cac tac aag gaa gca gcg ctt ggc atc atc gac   595
Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp
150                 155                 160                 165

ggt ggt ggc gat gcc ttt ttg att gag act gct cag gac ttg ctt cag   643
Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln
                170                 175                 180

gtc aag gct gcg gtt cac ggc gtt caa gat gcc atg gct gaa ctt gat   691
```

Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp
185 190 195

aca ttc ttg ccc att att tgc cac gtc acc gta gag acc acc ggc acc 739
Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr
200 205 210

atg ctc atg ggt tct gag atc ggt gcc gcg ttg aca gcg ctg cag cca 787
Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro
215 220 225

ctg ggt atc gac atg att ggt ctg aac tgc gcc acc ggc cca gat gag 835
Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu
230 235 240 245

atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtg 883
Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val
250 255 260

tcg gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca 931
Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala
265 270 275

gaa tac cca ctt gag gct gag gat ttg gcg cag gcg ctg gct gga ttc 979
Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe
280 285 290

gtc tcc gaa tat ggc ctg tcc atg gtg ggt ggt tgt tgt ggc acc aca 1027
Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr
295 300 305

cct gag cac atc cgt gcg gtc cgc gat gcg gtg gtt ggt gtt cca gag 1075
Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu
310 315 320 325

cag gaa acc tcc aca ctg acc aag atc cct gca ggc cct gtt gag cag 1123
Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln
330 335 340

gcc tcc cgc gag gtg gag aaa gag gac tcc gtc gcg tcg ctg tac acc 1171
Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr
345 350 355

tcg gtg cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc 1219
Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg
360 365 370

acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc 1267
Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly
375 380 385

gat tgg gaa aag tgt gtg gat att gcc aag cag caa acc cgc gat ggt 1315
Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly
390 395 400 405

gca cac atg ctg gat ctt tgt gtg gat tac gtg gga cga gac ggc acc 1363
Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr
410 415 420

gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg 1411
Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu

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              425                     430                     435

cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt      1459
Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu
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gag cac ttg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac      1507
Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp
    455                     460                     465

ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag      1555
Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys
470                     475                     480                 485

cag cac ggt gcg gcc gtg gtt gcg ctg acc att gat gag gaa ggc cag      1603
Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln
                490                     495                     500

gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac      1651
Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp
            505                     510                     515

gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac      1699
Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp
        520                     525                     530

tgc ctg acc ttc ccg atc tct act ggc cag gaa gaa acc agg cga gat      1747
Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp
    535                     540                     545

ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctc tac cca      1795
Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro
550                     555                     560                 565

gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac      1843
Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn
                570                     575                     580

cct gct gca cgc cag gtt ctt aac tct gtg ttc ctc aat gag tgc att      1891
Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile
            585                     590                     595

gag gct ggt ctg gac tct gcg att gcg cac agc tcc aag att ttg ccg      1939
Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro
        600                     605                     610

atg aac cgc att gat gat cgc cag cgc gaa gtg gcg ttg gat atg gtc      1987
Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val
    615                     620                     625

tat gat cgc cgc acc gag gat tac gat ccg ctg cag gaa ttc atg cag      2035
Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln
630                     635                     640                 645

ctg ttt gag ggc gtt tct gct gcc gat gcc aag gat gct cgc gct gaa      2083
Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu
                650                     655                     660

cag ctg gcc gct atg cct ttg ttt gag cgt ttg gca cag cgc atc atc      2131
Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile
            665                     670                     675
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gac ggc gat aag aat ggc ctt gag gat gat ctg gaa gca ggc atg aag   2179
Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys
        680                 685                 690

gag aag tct cct att gcg atc atc aac gag gac ctt ctc aac ggc atg   2227
Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met
    695                 700                 705

aag acc gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc   2275
Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe
710                 715                 720                 725

gtg ctg caa tcg gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa   2323
Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu
                730                 735                 740

ccg ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag   2371
Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu
            745                 750                 755

ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat   2419
Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp
        760                 765                 770

atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac   2467
Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp
    775                 780                 785

gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca   2515
Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala
790                 795                 800                 805

gcg gaa gaa cac aaa gca gac gtc atc ggc atg tcg gga ctt ctt gtg   2563
Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val
                810                 815                 820

aag tcc acc gtg gtg atg aag caa acc atc agc gac                   2599
Lys Ser Thr Val Val Met Lys Gln Thr Ile Ser Asp
            825                 830
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            20                  25                  30

Met Gly Thr Gln Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe
        35                  40                  45

Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp
    50                  55                  60

Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu
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65 70 75 80

Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr
85 90 95

Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val
100 105 110

Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg
115 120 125

Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu
130 135 140

Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala
145 150 155 160

Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala
165 170 175

Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala
180 185 190

Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val
195 200 205

Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu
210 215 220

Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala
225 230 235 240

Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His
245 250 255

Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu
260 265 270

Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln
275 280 285

Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly
290 295 300

Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val
305 310 315 320

Val Gly Val Pro Glu Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala
325 330 335

Gly Pro Val Glu Gln Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val
340 345 350

Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser
355 360 365

Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu
370 375 380

Ala Met Leu Ser Gly Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln
385 390 395 400

Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val
405 410 415

Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala
420 425 430

Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val
435 440 445

Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser
450 455 460

Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile
465 470 475 480

Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile
485 490 495

Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala
500 505 510

Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys
515 520 525

Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu
530 535 540

Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu
545 550 555 560

Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile
565 570 575

Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe
580 585 590

Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser
595 600 605

Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
610 615 620

Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu
625 630 635 640

Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys
645 650 655

Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu
660 665 670

Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu
675 680 685

Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp
690 695 700

Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln
705 710 715 720

Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala
725 730 735

Val Ala Tyr Leu Glu Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly
740 745 750

Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys
755 760 765

Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser
770 775 780

Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser
785 790 795 800

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805 810 815

Ser Gly Leu Leu Val Lys Ser Thr Val Val Met Lys Gln Thr Ile Ser
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Met Ser Thr Ser Val
1 5

act tca cca gcc cac aac aac gca cat tcc tcc gaa ttt ttg gat gcg 163
Thr Ser Pro Ala His Asn Asn Ala His Ser Ser Glu Phe Leu Asp Ala
10 15 20

ttg gca aac cat gtg ttg atc ggc gac ggc gcc atg ggc acc cag ctc 211
Leu Ala Asn His Val Leu Ile Gly Asp Gly Ala Met Gly Thr Gln Leu
25 30 35

caa ggc ttt gac ctg gac gtg gaa aag gat ttc ctt gat ctg gag ggg 259
Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe Leu Asp Leu Glu Gly
40 45 50

tgt aat gag att ctc aac gac acc cgc cct gat gtg ttg agg cag att 307
Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp Val Leu Arg Gln Ile
55 60 65

cac cgc gcc tac ttt gag gcg gga gct gac ttg gtt gag acc aat act 355
His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu Val Glu Thr Asn Thr
70 75 80 85

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ttt ggt tgc aac ctg ccg aac ttg gcg gat tat gac atc gct gat cgt   403
Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr Asp Ile Ala Asp Arg
             90                  95                  100

tgc cgt gag ctt gcc tac aag ggc act gca gtg gct agg gaa gtg gct   451
Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val Ala Arg Glu Val Ala
        105                 110                 115

gat gag atg ggg ccg ggc cga aac ggc atg cgg cgt ttc gtg gtt ggt   499
Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg Arg Phe Val Val Gly
    120                 125                 130

tcc ctg gga cct gga acg aag ctt cca tcg ctg ggc cat gca ccg tat   547
Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu Gly His Ala Pro Tyr
135                 140                 145

gca gat ttg cgt ggg cac tac aag gaa gca gcg ctt ggc atc atc gac   595
Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala Leu Gly Ile Ile Asp
150                 155                 160                 165

ggt ggt ggc gat gcc ttt ttg att gag act gct cag gac ttg ctt cag   643
Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala Gln Asp Leu Leu Gln
            170                 175                 180

gtc aag gct gcg gtt cac ggc gtt caa gat gcc atg gct gaa ctt gat   691
Val Lys Ala Ala Val His Gly Val Gln Asp Ala Met Ala Glu Leu Asp
        185                 190                 195

aca ttc ttg ccc att att tgc cac gtc acc gta gag acc acc ggc acc   739
Thr Phe Leu Pro Ile Ile Cys His Val Thr Val Glu Thr Thr Gly Thr
    200                 205                 210

atg ctc atg ggt tct gag atc ggt gcc gcg ttg aca gcg ctg cag cca   787
Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu Thr Ala Leu Gln Pro
215                 220                 225

ctg ggt atc gac atg att ggt ctg aac tgc gcc acc ggc cca gat gag   835
Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala Thr Gly Pro Asp Glu
230                 235                 240                 245

atg agc gag cac ctg cgt tac ctg tcc aag cac gcc gat att cct gtg   883
Met Ser Glu His Leu Arg Tyr Leu Ser Lys His Ala Asp Ile Pro Val
                250                 255                 260

tcg gtg atg cct aac gca ggt ctt cct gtc ctg ggt aaa aac ggt gca   931
Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu Gly Lys Asn Gly Ala
            265                 270                 275

gaa tac cca ctt gag gct gag gat ttg gcg cag gcg ctg gct gga ttc   979
Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln Ala Leu Ala Gly Phe
        280                 285                 290

gtc tcc gaa tat ggc ctg tcc atg gtg ggt ggt tgt tgt ggc acc aca   1027
Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly Cys Cys Gly Thr Thr
    295                 300                 305

cct gag cac atc cgt gcg gtc cgc gat gcg gtg gtt ggt gtt cca gag   1075
Pro Glu His Ile Arg Ala Val Arg Asp Ala Val Val Gly Val Pro Glu
310                 315                 320                 325
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cag gaa acc tcc aca ctg acc aag atc cct gca ggc cct gtt gag cag 1123
Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala Gly Pro Val Glu Gln
330 335 340

gcc tcc cgc gag gtg gag aaa gag gac tcc gtc gcg tcg ctg tac acc 1171
Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val Ala Ser Leu Tyr Thr
345 350 355

tcg gtg cca ttg tcc cag gaa acc ggc att tcc atg atc ggt gag cgc 1219
Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser Met Ile Gly Glu Arg
360 365 370

acc aac tcc aac ggt tcc aag gca ttc cgt gag gca atg ctg tct ggc 1267
Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu Ala Met Leu Ser Gly
375 380 385

gat tgg gaa aag tgt gtg gat att gcc aag cag caa acc cgc gat ggt 1315
Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln Gln Thr Arg Asp Gly
390 395 400 405

gca cac atg ctg gat ctt tgt gtg gat tac gtg gga cga gac ggc acc 1363
Ala His Met Leu Asp Leu Cys Val Asp Tyr Val Gly Arg Asp Gly Thr
410 415 420

gcc gat atg gcg acc ttg gca gca ctt ctt gct acc agc tcc act ttg 1411
Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala Thr Ser Ser Thr Leu
425 430 435

cca atc atg att gac tcc acc gag cca gag gtt att cgc aca ggc ctt 1459
Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val Ile Arg Thr Gly Leu
440 445 450

gag cac ttg ggt gga cga agc atc gtt aac tcc gtc aac ttt gaa gac 1507
Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser Val Asn Phe Glu Asp
455 460 465

ggc gat ggc cct gag tcc cgc tac cag cgc atc atg aaa ctg gta aag 1555
Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile Met Lys Leu Val Lys
470 475 480 485

cag cac ggt gcg gcc gtg gtt gcg ctg acc att gat gag gaa ggc cag 1603
Gln His Gly Ala Ala Val Val Ala Leu Thr Ile Asp Glu Glu Gly Gln
490 495 500

gca cgt acc gct gag cac aag gtg cgc att gct aaa cga ctg att gac 1651
Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala Lys Arg Leu Ile Asp
505 510 515

gat atc acc ggc agc tac ggc ctg gat atc aaa gac atc gtt gtg gac 1699
Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys Asp Ile Val Val Asp
520 525 530

tgc ctg acc ttc ccg atc tct act ggc cag gaa gaa acc agg cga gat 1747
Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu Glu Thr Arg Arg Asp
535 540 545

ggc att gaa acc atc gaa gcc atc cgc gag ctg aag aag ctc tac cca 1795
Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu Lys Lys Leu Tyr Pro
550 555 560 565

gaa atc cac acc acc ctg ggt ctg tcc aat att tcc ttc ggc ctg aac 1843

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Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile Ser Phe Gly Leu Asn
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cct gct gca cgc cag gtt ctt aac tct gtg ttc ctc aat gag tgc att   1891
Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe Leu Asn Glu Cys Ile
            585                 590                 595

gag gct ggt ctg gac tct gcg att gcg cac agc tcc aag att ttg ccg   1939
Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser Ser Lys Ile Leu Pro
        600                 605                 610

atg aac cgc att gat gat cgc cag cgc gaa gtg gcg ttg gat atg gtc   1987
Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val Ala Leu Asp Met Val
    615                 620                 625

tat gat cgc cgc acc gag gat tac gat ccg ctg cag gaa ttc atg cag   2035
Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu Gln Glu Phe Met Gln
630                 635                 640                 645

ctg ttt gag ggc gtt tct gct gcc gat gcc aag gat gct cgc gct gaa   2083
Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys Asp Ala Arg Ala Glu
                650                 655                 660

cag ctg gcc gct atg cct ttg ttt gag cgt ttg gca cag cgc atc atc   2131
Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu Ala Gln Arg Ile Ile
            665                 670                 675

gac ggc gat aag aat ggc ctt gag gat gat ctg gaa gca ggc atg aag   2179
Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu Glu Ala Gly Met Lys
        680                 685                 690

gag aag tct cct att gcg atc atc aac gag gac ctt ctc aac ggc atg   2227
Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp Leu Leu Asn Gly Met
    695                 700                 705

aag acc gtg ggt gag ctg ttt ggt tcc gga cag atg cag ctg cca ttc   2275
Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln Met Gln Leu Pro Phe
710                 715                 720                 725

gtg ctg caa tcg gca gaa acc atg aaa act gcg gtg gcc tat ttg gaa   2323
Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala Val Ala Tyr Leu Glu
                730                 735                 740

ccg ttc atg gaa gag gaa gca gaa gct acc gga tct gcg cag gca gag   2371
Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly Ser Ala Gln Ala Glu
            745                 750                 755

ggc aag ggc aaa atc gtc gtg gcc acc gtc aag ggt gac gtg cac gat   2419
Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys Gly Asp Val His Asp
        760                 765                 770

atc ggc aag aac ttg gtg gac atc att ttg tcc aac aac ggt tac gac   2467
Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser Asn Asn Gly Tyr Asp
    775                 780                 785

gtg gtg aac ttg ggc atc aag cag cca ctg tcc gcc atg ttg gaa gca   2515
Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser Ala Met Leu Glu Ala
790                 795                 800                 805

gcg gaa gaa cac aaa gca gac gtc atc ggc atg tcg gga ctt ctt gtg   2563
Ala Glu Glu His Lys Ala Asp Val Ile Gly Met Ser Gly Leu Leu Val
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810 815 820

aag tcc acc gtg gtg 2578
Lys Ser Thr Val Val
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20 25 30

Met Gly Thr Gln Leu Gln Gly Phe Asp Leu Asp Val Glu Lys Asp Phe
35 40 45

Leu Asp Leu Glu Gly Cys Asn Glu Ile Leu Asn Asp Thr Arg Pro Asp
50 55 60

Val Leu Arg Gln Ile His Arg Ala Tyr Phe Glu Ala Gly Ala Asp Leu
65 70 75 80

Val Glu Thr Asn Thr Phe Gly Cys Asn Leu Pro Asn Leu Ala Asp Tyr
85 90 95

Asp Ile Ala Asp Arg Cys Arg Glu Leu Ala Tyr Lys Gly Thr Ala Val
100 105 110

Ala Arg Glu Val Ala Asp Glu Met Gly Pro Gly Arg Asn Gly Met Arg
115 120 125

Arg Phe Val Val Gly Ser Leu Gly Pro Gly Thr Lys Leu Pro Ser Leu
130 135 140

Gly His Ala Pro Tyr Ala Asp Leu Arg Gly His Tyr Lys Glu Ala Ala
145 150 155 160

Leu Gly Ile Ile Asp Gly Gly Gly Asp Ala Phe Leu Ile Glu Thr Ala
165 170 175

Gln Asp Leu Leu Gln Val Lys Ala Ala Val His Gly Val Gln Asp Ala
180 185 190

Met Ala Glu Leu Asp Thr Phe Leu Pro Ile Ile Cys His Val Thr Val
195 200 205

Glu Thr Thr Gly Thr Met Leu Met Gly Ser Glu Ile Gly Ala Ala Leu
210 215 220

Thr Ala Leu Gln Pro Leu Gly Ile Asp Met Ile Gly Leu Asn Cys Ala
225 230 235 240

Thr Gly Pro Asp Glu Met Ser Glu His Leu Arg Tyr Leu Ser Lys His
245 250 255

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Ala Asp Ile Pro Val Ser Val Met Pro Asn Ala Gly Leu Pro Val Leu
            260                 265                 270

Gly Lys Asn Gly Ala Glu Tyr Pro Leu Glu Ala Glu Asp Leu Ala Gln
        275                 280                 285

Ala Leu Ala Gly Phe Val Ser Glu Tyr Gly Leu Ser Met Val Gly Gly
    290                 295                 300

Cys Cys Gly Thr Thr Pro Glu His Ile Arg Ala Val Arg Asp Ala Val
305                 310                 315                 320

Val Gly Val Pro Glu Gln Glu Thr Ser Thr Leu Thr Lys Ile Pro Ala
                325                 330                 335

Gly Pro Val Glu Gln Ala Ser Arg Glu Val Glu Lys Glu Asp Ser Val
            340                 345                 350

Ala Ser Leu Tyr Thr Ser Val Pro Leu Ser Gln Glu Thr Gly Ile Ser
        355                 360                 365

Met Ile Gly Glu Arg Thr Asn Ser Asn Gly Ser Lys Ala Phe Arg Glu
    370                 375                 380

Ala Met Leu Ser Gly Asp Trp Glu Lys Cys Val Asp Ile Ala Lys Gln
385                 390                 395                 400

Gln Thr Arg Asp Gly Ala His Met Leu Asp Leu Cys Val Asp Tyr Val
                405                 410                 415

Gly Arg Asp Gly Thr Ala Asp Met Ala Thr Leu Ala Ala Leu Leu Ala
            420                 425                 430

Thr Ser Ser Thr Leu Pro Ile Met Ile Asp Ser Thr Glu Pro Glu Val
        435                 440                 445

Ile Arg Thr Gly Leu Glu His Leu Gly Gly Arg Ser Ile Val Asn Ser
    450                 455                 460

Val Asn Phe Glu Asp Gly Asp Gly Pro Glu Ser Arg Tyr Gln Arg Ile
465                 470                 475                 480

Met Lys Leu Val Lys Gln His Gly Ala Ala Val Val Ala Leu Thr Ile
                485                 490                 495

Asp Glu Glu Gly Gln Ala Arg Thr Ala Glu His Lys Val Arg Ile Ala
            500                 505                 510

Lys Arg Leu Ile Asp Asp Ile Thr Gly Ser Tyr Gly Leu Asp Ile Lys
        515                 520                 525

Asp Ile Val Val Asp Cys Leu Thr Phe Pro Ile Ser Thr Gly Gln Glu
    530                 535                 540

Glu Thr Arg Arg Asp Gly Ile Glu Thr Ile Glu Ala Ile Arg Glu Leu
545                 550                 555                 560

Lys Lys Leu Tyr Pro Glu Ile His Thr Thr Leu Gly Leu Ser Asn Ile
                565                 570                 575

Ser Phe Gly Leu Asn Pro Ala Ala Arg Gln Val Leu Asn Ser Val Phe
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580 585 590

Leu Asn Glu Cys Ile Glu Ala Gly Leu Asp Ser Ala Ile Ala His Ser
595 600 605

Ser Lys Ile Leu Pro Met Asn Arg Ile Asp Asp Arg Gln Arg Glu Val
610 615 620

Ala Leu Asp Met Val Tyr Asp Arg Arg Thr Glu Asp Tyr Asp Pro Leu
625 630 635 640

Gln Glu Phe Met Gln Leu Phe Glu Gly Val Ser Ala Ala Asp Ala Lys
645 650 655

Asp Ala Arg Ala Glu Gln Leu Ala Ala Met Pro Leu Phe Glu Arg Leu
660 665 670

Ala Gln Arg Ile Ile Asp Gly Asp Lys Asn Gly Leu Glu Asp Asp Leu
675 680 685

Glu Ala Gly Met Lys Glu Lys Ser Pro Ile Ala Ile Ile Asn Glu Asp
690 695 700

Leu Leu Asn Gly Met Lys Thr Val Gly Glu Leu Phe Gly Ser Gly Gln
705 710 715 720

Met Gln Leu Pro Phe Val Leu Gln Ser Ala Glu Thr Met Lys Thr Ala
725 730 735

Val Ala Tyr Leu Glu Pro Phe Met Glu Glu Glu Ala Glu Ala Thr Gly
740 745 750

Ser Ala Gln Ala Glu Gly Lys Gly Lys Ile Val Val Ala Thr Val Lys
755 760 765

Gly Asp Val His Asp Ile Gly Lys Asn Leu Val Asp Ile Ile Leu Ser
770 775 780

Asn Asn Gly Tyr Asp Val Val Asn Leu Gly Ile Lys Gln Pro Leu Ser
785 790 795 800

Ala Met Leu Glu Ala Ala Glu Glu His Lys Ala Asp Val Ile Gly Met
805 810 815

Ser Gly Leu Leu Val Lys Ser Thr Val Val
820 825

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<223> RXN03074

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tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct 115
Met Thr Gln Ser Ala
1 5

cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac 163
Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
10 15 20

gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa 211
Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
25 30 35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc 259
Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
40 45 50

ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc 307
Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
55 60 65

gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
70 75 80 85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
90 95 100

att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
105 110 115

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
120 125 130

gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
135 140 145

gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
150 155 160 165

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Gln

<210> 94
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<212> PRT
<213> Corynebacterium glutamicum

<400> 94
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Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
20 25 30

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Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
        35                  40                  45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
    50                  55                  60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
65                  70                  75                  80

Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
                85                  90                  95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
            100                 105                 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
        115                 120                 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
    130                 135                 140

Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
145                 150                 155                 160

Glu Ala Pro Ile Lys Gln
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tagcaggaca agcatactgt tttagttcta tgctgtgggc atg act caa agt gct    115
                                            Met Thr Gln Ser Ala
                                            1               5

cca gaa ttc att gcc acc gca gac ctc gta gac atc atc ggc gac aac    163
Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp Ile Ile Gly Asp Asn
                10                  15                  20

gcg caa tca tgc gac act cag ttt caa aac ctt gga ggt gcc aca gaa    211
Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu Gly Gly Ala Thr Glu
            25                  30                  35

ttc cac gga ata ata acc acc gtg aaa tgc ttc caa gac aac gcc ctc    259
Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe Gln Asp Asn Ala Leu
        40                  45                  50

ctg aaa tcc atc ctg agc gag gat aat cct ggg gga gtg ctg gtt atc    307
Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly Gly Val Leu Val Ile
    55                  60                  65
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gat ggc gac gca tcc gtg cac acc gcg cta gtt ggc gac atc att gca 355
Asp Gly Asp Ala Ser Val His Thr Ala Leu Val Gly Asp Ile Ile Ala
70 75 80 85

gga ctt gga aaa gat cat ggt tgg tcc gga gta att gtc aac gga gca 403
Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val Ile Val Asn Gly Ala
90 95 100

att cga gac tcc gca gtc atc ggc acc atg acc ttt ggt tgt aaa gcc 451
Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr Phe Gly Cys Lys Ala
105 110 115

ctt gga acc aac ccg cgg aaa tcc act aaa act ggt tcc ggc gaa cga 499
Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr Gly Ser Gly Glu Arg
120 125 130

gac gta gtg gta tcg att ggt ggc att gac ttc att cct ggt cat tac 547
Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe Ile Pro Gly His Tyr
135 140 145

gtc tac gcg gac tct gac gga att atc gtc acc gag gcg cca att aag 595
Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr Glu Ala Pro Ile Lys
150 155 160 165

cag taatttgttt tgacgacgca gta 621
Gln

<210> 96
<211> 166
<212> PRT
<213> Corynebacterium glutamicum

<400> 96
Met Thr Gln Ser Ala Pro Glu Phe Ile Ala Thr Ala Asp Leu Val Asp
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Ile Ile Gly Asp Asn Ala Gln Ser Cys Asp Thr Gln Phe Gln Asn Leu
20 25 30

Gly Gly Ala Thr Glu Phe His Gly Ile Ile Thr Thr Val Lys Cys Phe
35 40 45

Gln Asp Asn Ala Leu Leu Lys Ser Ile Leu Ser Glu Asp Asn Pro Gly
50 55 60

Gly Val Leu Val Ile Asp Gly Asp Ala Ser Val His Thr Ala Leu Val
65 70 75 80

Gly Asp Ile Ile Ala Gly Leu Gly Lys Asp His Gly Trp Ser Gly Val
85 90 95

Ile Val Asn Gly Ala Ile Arg Asp Ser Ala Val Ile Gly Thr Met Thr
100 105 110

Phe Gly Cys Lys Ala Leu Gly Thr Asn Pro Arg Lys Ser Thr Lys Thr
115 120 125

Gly Ser Gly Glu Arg Asp Val Val Val Ser Ile Gly Gly Ile Asp Phe
130 135 140

Ile Pro Gly His Tyr Val Tyr Ala Asp Ser Asp Gly Ile Ile Val Thr
145 150 155 160

Glu Ala Pro Ile Lys Gln
165

<210> 97
<211> 1557
<212> DNA
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<220>
<221> CDS
<222> (101)..(1534)
<223> RXN00132

<400> 97
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tttcctaatt ttcattttct taaaaggagc tcgccaggac atg gca cag gtt atg 115
Met Ala Gln Val Met
1 5

gac ttc aag gtt gcc gat ctt tca cta gca gag gca gga cgt cac cag 163
Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu Ala Gly Arg His Gln
10 15 20

att cgt ctt gca gag tat gag atg cca ggt ctc atg cag ttg cgc aag 211
Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu Met Gln Leu Arg Lys
25 30 35

gaa ttc gca gac gag cag cct ttg aag ggc gcc cga att gct ggt tct 259
Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala Arg Ile Ala Gly Ser
40 45 50

atc cac atg acg gtc cag acc gcc gtg ctt att gag acc ctc act gct 307
Ile His Met Thr Val Gln Thr Ala Val Leu Ile Glu Thr Leu Thr Ala
55 60 65

ttg ggc gct gag gtt cgt tgg gct tcc tgc aac att ttc tcc acc cag 355
Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn Ile Phe Ser Thr Gln
70 75 80 85

gat gag gct gca gcg gct atc gtt gtc ggc tcc ggc acc gtc gaa gag 403
Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser Gly Thr Val Glu Glu
90 95 100

cca gct ggt gtt cca gta ttc gcg tgg aag ggt gag tca ctg gag gag 451
Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly Glu Ser Leu Glu Glu
105 110 115

tac tgg tgg tgc atc aac cag atc ttc agc tgg ggc gat gag ctg cca 499
Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp Gly Asp Glu Leu Pro
120 125 130

aac atg atc ctc gac gac ggc ggt gac gcc acc atg gct gtt att cgc 547
Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr Met Ala Val Ile Arg
135 140 145

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ggt cgc gaa tac gag cag gct ggt ctg gtt cca cca gca gag gcc aac   595
Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro Pro Ala Glu Ala Asn
150                 155                 160                 165

gat tcc gat gag tac atc gca ttc ttg ggc atg ctg cgt gag gtt ctt   643
Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met Leu Arg Glu Val Leu
                170                 175                 180

gct gca gag cct ggc aag tgg ggc aag atc gct gag gcc gtt aag ggt   691
Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala Glu Ala Val Lys Gly
            185                 190                 195

gtc acc gag gaa acc acc acc ggt gtg cac cgc ctg tac cac ttc gct   739
Val Thr Glu Glu Thr Thr Thr Gly Val His Arg Leu Tyr His Phe Ala
        200                 205                 210

gaa gaa ggc gtg ctg cct ttc cca gcg atg aac gtc aac gac gct gtc   787
Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn Val Asn Asp Ala Val
    215                 220                 225

acc aag tcc aag ttt gat aac aag tac ggc acc cgc cac tcc ctg atc   835
Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr Arg His Ser Leu Ile
230                 235                 240                 245

gac ggc atc aac cgc gcc act gac atg ctc atg ggc ggc aag aac gtg   883
Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met Gly Gly Lys Asn Val
                250                 255                 260

ctt gtc tgc ggt tac ggc gat gtc ggc aag ggc tgc gct gag gct ttc   931
Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Glu Ala Phe
            265                 270                 275

gac ggc cag ggc gct cgc gtc aag gtc acc gaa gct gac cca atc aac   979
Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn
        280                 285                 290

gct ctt cag gct ctg atg gat ggc tac tct gtg gtc acc gtt gat gag   1027
Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu
    295                 300                 305

gcc atc gag gac gcc gac atc gtg atc acc gcg acc ggc aac aag gac   1075
Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala Thr Gly Asn Lys Asp
310                 315                 320                 325

atc att tcc ttc gag cag atg ctc aag atg aag gat cac gct ctg ctg   1123
Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys Asp His Ala Leu Leu
                330                 335                 340

ggc aac atc ggt cac ttt gat aat gag atc gat atg cat tcc ctg ttg   1171
Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu
            345                 350                 355

cac cgc gac gac gtc acc cgc acc acg atc aag cca cag gtc gac gag   1219
His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu
        360                 365                 370

ttc acc ttc tcc acc ggt cgc tcc atc atc gtc ctg tcc gaa ggt cgc   1267
Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg
    375                 380                 385

ctg ttg aac ctt ggc aac gcc acc gga cac cca tca ttt gtc atg tcc   1315
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Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser
390 395 400 405

aac tct ttc gcc gat cag acc att gcg cag atc gaa ctg ttc caa aac 1363
Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn
410 415 420

gaa gga cag tac gag aac gag gtc tac cgt ctg cct aag gtt ctc gac 1411
Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu Pro Lys Val Leu Asp
425 430 435

gaa aag gtg gca cgc atc cac gtt gag gct ctc ggc ggt cag ctc acc 1459
Glu Lys Val Ala Arg Ile His Val Glu Ala Leu Gly Gly Gln Leu Thr
440 445 450

gaa ctg acc aag gag cag gct gag tac atc ggc gtt gac gtt gca ggc 1507
Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly Val Asp Val Ala Gly
455 460 465

cca ttc aag ccg gag cac tac cgc tac taatgattgt cagcattgag gga 1557
Pro Phe Lys Pro Glu His Tyr Arg Tyr
470 475

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<211> 478
<212> PRT
<213> Corynebacterium glutamicum

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Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu
20 25 30

Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala
35 40 45

Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile
50 55 60

Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn
65 70 75 80

Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser
85 90 95

Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly
100 105 110

Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp
115 120 125

Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr
130 135 140

Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro
145 150 155 160

Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met

165 170 175

Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala
180 185 190

Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg
195 200 205

Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn
210 215 220

Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr
225 230 235 240

Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met
245 250 255

Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly
260 265 270

Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu
275 280 285

Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val
290 295 300

Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala
305 310 315 320

Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys
325 330 335

Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp
340 345 350

Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys
355 360 365

Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val
370 375 380

Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro
385 390 395 400

Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile
405 410 415

Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu
420 425 430

Pro Lys Val Leu Asp Glu Lys Val Ala Arg Ile His Val Glu Ala Leu
435 440 445

Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln Ala Glu Tyr Ile Gly
450 455 460

Val Asp Val Ala Gly Pro Phe Lys Pro Glu His Tyr Arg Tyr
465 470 475

<210> 99

<211> 128
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (1)..(105)
<223> FRXA00132

<400> 99
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His Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln
1 5 10 15

gct gag tac atc ggc gtt gac gtt gca ggc cca ttc aag ccg gag cac 96
Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His
20 25 30

tac cgc tac taatgattgt cagcattgag gga 128
Tyr Arg Tyr
35

<210> 100
<211> 35
<212> PRT
<213> Corynebacterium glutamicum

<400> 100
His Val Glu Ala Leu Gly Gly Gln Leu Thr Glu Leu Thr Lys Glu Gln
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Ala Glu Tyr Ile Gly Val Asp Val Ala Gly Pro Phe Lys Pro Glu His
20 25 30

Tyr Arg Tyr
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<210> 101
<211> 1396
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1396)
<223> FRXA01371

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tttcctaatt ttcattttct taaaaggagc tcgccaggac atg gca cag gtt atg 115
Met Ala Gln Val Met
1 5

gac ttc aag gtt gcc gat ctt tca cta gca gag gca gga cgt cac cag 163
Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu Ala Gly Arg His Gln
10 15 20

att cgt ctt gca gag tat gag atg cca ggt ctc atg cag ttg cgc aag 211

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Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu Met Gln Leu Arg Lys
            25                  30                  35

gaa ttc gca gac gag cag cct ttg aag ggc gcc cga att gct ggt tct     259
Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala Arg Ile Ala Gly Ser
        40                  45                  50

atc cac atg acg gtc cag acc gcc gtg ctt att gag acc ctc act gct     307
Ile His Met Thr Val Gln Thr Ala Val Leu Ile Glu Thr Leu Thr Ala
    55                  60                  65

ttg ggc gct gag gtt cgt tgg gct tcc tgc aac att ttc tcc acc cag     355
Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn Ile Phe Ser Thr Gln
70                  75                  80                  85

gat gag gct gca gcg gct atc gtt gtc ggc tcc ggc acc gtc gaa gag     403
Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser Gly Thr Val Glu Glu
                90                  95                  100

cca gct ggt gtt cca gta ttc gcg tgg aag ggt gag tca ctg gag gag     451
Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly Glu Ser Leu Glu Glu
            105                 110                 115

tac tgg tgg tgc atc aac cag atc ttc agc tgg ggc gat gag ctg cca     499
Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp Gly Asp Glu Leu Pro
        120                 125                 130

aac atg atc ctc gac gac ggc ggt gac gcc acc atg gct gtt att cgc     547
Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr Met Ala Val Ile Arg
    135                 140                 145

ggt cgc gaa tac gag cag gct ggt ctg gtt cca cca gca gag gcc aac     595
Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro Pro Ala Glu Ala Asn
150                 155                 160                 165

gat tcc gat gag tac atc gca ttc ttg ggc atg ctg cgt gag gtt ctt     643
Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met Leu Arg Glu Val Leu
                170                 175                 180

gct gca gag cct ggc aag tgg ggc aag atc gct gag gcc gtt aag ggt     691
Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala Glu Ala Val Lys Gly
            185                 190                 195

gtc acc gag gaa acc acc acc ggt gtg cac cgc ctg tac cac ttc gct     739
Val Thr Glu Glu Thr Thr Thr Gly Val His Arg Leu Tyr His Phe Ala
        200                 205                 210

gaa gaa ggc gtg ctg cct ttc cca gcg atg aac gtc aac gac gct gtc     787
Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn Val Asn Asp Ala Val
    215                 220                 225

acc aag tcc aag ttt gat aac aag tac ggc acc cgc cac tcc ctg atc     835
Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr Arg His Ser Leu Ile
230                 235                 240                 245

gac ggc atc aac cgc gcc act gac atg ctc atg ggc ggc aag aac gtg     883
Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met Gly Gly Lys Asn Val
                250                 255                 260

ctt gtc tgc ggt tac ggc gat gtc ggc aag ggc tgc gct gag gct ttc     931
Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly Cys Ala Glu Ala Phe
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            265                 270                 275

gac ggc cag ggc gct cgc gtc aag gtc acc gaa gct gac cca atc aac   979
Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu Ala Asp Pro Ile Asn
        280                 285                 290

gct ctt cag gct ctg atg gat ggc tac tct gtg gtc acc gtt gat gag   1027
Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val Val Thr Val Asp Glu
    295                 300                 305

gcc atc gag gac gcc gac atc gtg atc acc gcg acc ggc aac aag gac   1075
Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala Thr Gly Asn Lys Asp
310                 315                 320                 325

atc att tcc ttc gag cag atg ctc aag atg aag gat cac gct ctg ctg   1123
Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys Asp His Ala Leu Leu
                330                 335                 340

ggc aac atc ggt cac ttt gat aat gag atc gat atg cat tcc ctg ttg   1171
Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp Met His Ser Leu Leu
            345                 350                 355

cac cgc gac gac gtc acc cgc acc acg atc aag cca cag gtc gac gag   1219
His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys Pro Gln Val Asp Glu
        360                 365                 370

ttc acc ttc tcc acc ggt cgc tcc atc atc gtc ctg tcc gaa ggt cgc   1267
Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val Leu Ser Glu Gly Arg
    375                 380                 385

ctg ttg aac ctt ggc aac gcc acc gga cac cca tca ttt gtc atg tcc   1315
Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro Ser Phe Val Met Ser
390                 395                 400                 405

aac tct ttc gcc gat cag acc att gcg cag atc gaa ctg ttc caa aac   1363
Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile Glu Leu Phe Gln Asn
                410                 415                 420

gaa gga cag tac gag aac gag gtc tac cgt ctg                      1396
Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu
            425                 430


<210> 102
<211> 432
<212> PRT
<213> Corynebacterium glutamicum

<400> 102
Met Ala Gln Val Met Asp Phe Lys Val Ala Asp Leu Ser Leu Ala Glu
  1               5                  10                  15

Ala Gly Arg His Gln Ile Arg Leu Ala Glu Tyr Glu Met Pro Gly Leu
             20                  25                  30

Met Gln Leu Arg Lys Glu Phe Ala Asp Glu Gln Pro Leu Lys Gly Ala
         35                  40                  45

Arg Ile Ala Gly Ser Ile His Met Thr Val Gln Thr Ala Val Leu Ile
     50                  55                  60
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Glu Thr Leu Thr Ala Leu Gly Ala Glu Val Arg Trp Ala Ser Cys Asn
65 70 75 80

Ile Phe Ser Thr Gln Asp Glu Ala Ala Ala Ala Ile Val Val Gly Ser
85 90 95

Gly Thr Val Glu Glu Pro Ala Gly Val Pro Val Phe Ala Trp Lys Gly
100 105 110

Glu Ser Leu Glu Glu Tyr Trp Trp Cys Ile Asn Gln Ile Phe Ser Trp
115 120 125

Gly Asp Glu Leu Pro Asn Met Ile Leu Asp Asp Gly Gly Asp Ala Thr
130 135 140

Met Ala Val Ile Arg Gly Arg Glu Tyr Glu Gln Ala Gly Leu Val Pro
145 150 155 160

Pro Ala Glu Ala Asn Asp Ser Asp Glu Tyr Ile Ala Phe Leu Gly Met
165 170 175

Leu Arg Glu Val Leu Ala Ala Glu Pro Gly Lys Trp Gly Lys Ile Ala
180 185 190

Glu Ala Val Lys Gly Val Thr Glu Glu Thr Thr Thr Gly Val His Arg
195 200 205

Leu Tyr His Phe Ala Glu Glu Gly Val Leu Pro Phe Pro Ala Met Asn
210 215 220

Val Asn Asp Ala Val Thr Lys Ser Lys Phe Asp Asn Lys Tyr Gly Thr
225 230 235 240

Arg His Ser Leu Ile Asp Gly Ile Asn Arg Ala Thr Asp Met Leu Met
245 250 255

Gly Gly Lys Asn Val Leu Val Cys Gly Tyr Gly Asp Val Gly Lys Gly
260 265 270

Cys Ala Glu Ala Phe Asp Gly Gln Gly Ala Arg Val Lys Val Thr Glu
275 280 285

Ala Asp Pro Ile Asn Ala Leu Gln Ala Leu Met Asp Gly Tyr Ser Val
290 295 300

Val Thr Val Asp Glu Ala Ile Glu Asp Ala Asp Ile Val Ile Thr Ala
305 310 315 320

Thr Gly Asn Lys Asp Ile Ile Ser Phe Glu Gln Met Leu Lys Met Lys
325 330 335

Asp His Ala Leu Leu Gly Asn Ile Gly His Phe Asp Asn Glu Ile Asp
340 345 350

Met His Ser Leu Leu His Arg Asp Asp Val Thr Arg Thr Thr Ile Lys
355 360 365

Pro Gln Val Asp Glu Phe Thr Phe Ser Thr Gly Arg Ser Ile Ile Val
370 375 380

Leu Ser Glu Gly Arg Leu Leu Asn Leu Gly Asn Ala Thr Gly His Pro

385 390 395 400

Ser Phe Val Met Ser Asn Ser Phe Ala Asp Gln Thr Ile Ala Gln Ile
405 410 415

Glu Leu Phe Gln Asn Glu Gly Gln Tyr Glu Asn Glu Val Tyr Arg Leu
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Met Thr Ser Asn Phe
1 5

tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg 163
Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu
10 15 20

aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa 211
Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu
25 30 35

ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg 259
Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu
40 45 50

tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca 307
Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala
55 60 65

atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat 355
Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp
70 75 80 85

gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc 403
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg
90 95 100

tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg 451
Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met
105 110 115

acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct 499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser
120 125 130

gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc 547
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu
135 140 145

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cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt    595
Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly
150                 155                 160                 165

cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct    643
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro
                170                 175                 180

ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag    691
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys
            185                 190                 195

tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc    739
Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr
        200                 205                 210

gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act    787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr
    215                 220                 225

ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc    835
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly
230                 235                 240                 245

gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc    883
Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly
                250                 255                 260

gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt    931
Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly
            265                 270                 275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc    979
Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg
        280                 285                 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc    1027
Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg
    295                 300                 305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac    1075
Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr
310                 315                 320                 325

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc    1123
Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala
                330                 335                 340

ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta    1171
Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu
            345                 350                 355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att    1219
Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile
        360                 365                 370

gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc    1267
Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu
    375                 380                 385
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cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag     1315
Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu
390                 395                 400                 405

aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc     1363
Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe
                410                 415                 420

cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa     1411
Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu
            425                 430                 435

tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat     1459
Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp
        440                 445                 450

ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac     1507
Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His
    455                 460                 465

ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc     1555
Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu
470                 475                 480                 485

gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc     1603
Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser
                490                 495                 500

cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg     1651
Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala
            505                 510                 515

cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag     1699
Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys
        520                 525                 530

cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc     1747
His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
    535                 540                 545

ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca     1795
Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala
550                 555                 560                 565

ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag     1843
Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys
                570                 575                 580

atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccg cta cga     1891
Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Leu Arg
            585                 590                 595

gac gtc gat aag cct gcc tac ctg cag tgg tcc gtg gac tcc ttc cgc     1939
Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg
        600                 605                 610

ctg gcg act gcc ggc gca ccc gac gac gtc caa atc cac acc cac atg     1987
Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met
    615                 620                 625

tgc tac tcc gag ttc aac gaa gtg atc tcc tcg gtc atc gcg ttg gat     2035
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Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp
630 635 640 645

gcc gat gtc acc acc atc gaa gca gca cgt tcc gac atg cag gtc ctc 2083
Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu
650 655 660

gct gct ctg aaa tct tcc ggc ttc gag ctc ggc gtc gga cct ggt gtg 2131
Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val
665 670 675

tgg gat atc cac tcc ccg cgc gtt cct tcc gcg cag aaa gtg gac ggt 2179
Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly
680 685 690

ctc ctc gag gct gca ctg cag tcc gtg gat cct cgc cag ctg tgg gtc 2227
Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val
695 700 705

aac cca gac tgt ggt ctg aag acc cgt gga tgg cca gaa gtg gaa gct 2275
Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala
710 715 720 725

tcc cta aag gtt ctc gtt gag tcc gct aag cag gct cgt gag aaa atc 2323
Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile
730 735 740

gga gca act atc taaattgggt taccgctagg aac 2358
Gly Ala Thr Ile
745

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Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
35 40 45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
50 55 60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
65 70 75 80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
85 90 95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
100 105 110

Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
115 120 125

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Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
    130                 135                 140

Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
145                 150                 155                 160

Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
                165                 170                 175

Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
            180                 185                 190

Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
        195                 200                 205

Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
    210                 215                 220

Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
225                 230                 235                 240

Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
                245                 250                 255

Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
            260                 265                 270

Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
        275                 280                 285

Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
    290                 295                 300

Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
305                 310                 315                 320

Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
                325                 330                 335

Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
            340                 345                 350

Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala
        355                 360                 365

Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro
    370                 375                 380

Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
385                 390                 395                 400

Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
                405                 410                 415

Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala
            420                 425                 430

Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
        435                 440                 445
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Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
450 455 460

Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
465 470 475 480

Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val
485 490 495

Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
500 505 510

Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
515 520 525

Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
530 535 540

Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
545 550 555 560

Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
565 570 575

Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
580 585 590

Leu Leu Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln Trp Ser
595 600 605

Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp Val Gln
610 615 620

Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile Ser Ser
625 630 635 640

Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala Arg Ser
645 650 655

Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu Leu Gly
660 665 670

Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro Ser Ala
675 680 685

Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val Asp Pro
690 695 700

Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg Gly Trp
705 710 715 720

Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala Lys Gln
725 730 735

Ala Arg Glu Lys Ile Gly Ala Thr Ile
740 745

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<222> (101)..(1900)
<223> FRXA02085

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Met Thr Ser Asn Phe
1 5

tct tcc act gtc gct ggt ctt cct cgc atc gga gcg aag cgt gaa ctg 163
Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly Ala Lys Arg Glu Leu
10 15 20

aag ttc gcg ctc gaa ggc tac tgg aat gga tca att gaa ggt cgc gaa 211
Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser Ile Glu Gly Arg Glu
25 30 35

ctt gcg cag acc gcc cgc caa ttg gtc aac act gca tcg gat tct ttg 259
Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr Ala Ser Asp Ser Leu
40 45 50

tct gga ttg gat tcc gtt ccg ttt gca gga cgt tcc tac tac gac gca 307
Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg Ser Tyr Tyr Asp Ala
55 60 65

atg ctc gat acc gcc gct att ttg ggt gtg ctg ccg gag cgt ttt gat 355
Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu Pro Glu Arg Phe Asp
70 75 80 85

gac atc gct gat cat gaa aac gat ggt ctc cca ctg tgg att gac cgc 403
Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro Leu Trp Ile Asp Arg
90 95 100

tac ttt ggc gct gct cgc ggt act gag acc ctg cct gca cag gca atg 451
Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu Pro Ala Gln Ala Met
105 110 115

acc aag tgg ttt gat acc aac tac cac tac ctc gtg ccg gag ttg tct 499
Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu Val Pro Glu Leu Ser
120 125 130

gcg gat aca cgt ttc gtt ttg gat gcg tcc gcg ctg att gag gat ctc 547
Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala Leu Ile Glu Asp Leu
135 140 145

cgt tgc cag cag gtt cgt ggc gtt aat gcc cgc cct gtt ctg gtt ggt 595
Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg Pro Val Leu Val Gly
150 155 160 165

cca ctg act ttc ctt tcc ctt gct cgc acc act gat ggt tcc aat cct 643
Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr Asp Gly Ser Asn Pro
170 175 180

ttg gat cac ctg cct gca ctg ttt gag gtc tac gag cgc ctc atc aag 691
Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr Glu Arg Leu Ile Lys
185 190 195

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tct ttc gat act gag tgg gtt cag atc gat gag cct gcg ttg gtc acc   739
Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu Pro Ala Leu Val Thr
        200                 205                 210

gat gtt gct cct gag gtt ttg gag cag gtc cgc gct ggt tac acc act   787
Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg Ala Gly Tyr Thr Thr
    215                 220                 225

ttg gct aag cgc gat ggc gtg ttt gtc aat act tac ttc ggc tct ggc   835
Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr Tyr Phe Gly Ser Gly
230                 235                 240                 245

gat cag gcg ctg aac act ctt gcg ggc atc ggc ctt ggc gcg att ggc   883
Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly Leu Gly Ala Ile Gly
                250                 255                 260

gtt gac ttg gtc acc cat ggc gtc act gag ctt gct gcg tgg aag ggt   931
Val Asp Leu Val Thr His Gly Val Thr Glu Leu Ala Ala Trp Lys Gly
            265                 270                 275

gag gag ctg ctg gtt gcg ggc atc gtt gat ggt cgt aac att tgg cgc   979
Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly Arg Asn Ile Trp Arg
        280                 285                 290

acc gac ctg tgt gct gct ctt gct tcc ctg aag cgc ctg gca gct cgc   1027
Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys Arg Leu Ala Ala Arg
    295                 300                 305

ggc cca atc gca gtg tct acc tct tgt tca ctg ctg cac gtt cct tac   1075
Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu Leu His Val Pro Tyr
310                 315                 320                 325

acc ctc gag gct gag aac att gag cct gag gtc cgc gac tgg ctt gcc   1123
Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val Arg Asp Trp Leu Ala
                330                 335                 340

ttc ggc tcg gag aag atc acc gag gtc aag ctg ctt gcc gac gcc cta   1171
Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu Leu Ala Asp Ala Leu
            345                 350                 355

gcc ggc aac atc gac gcg gct gcg ttc gat gcg gcg tcc gca gca att   1219
Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala Ala Ser Ala Ala Ile
        360                 365                 370

gct tct cga cgc acc tcc cca cgc acc gca cca atc acg cag gaa ctc   1267
Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro Ile Thr Gln Glu Leu
    375                 380                 385

cct ggc cgt agc cgt gga tcc ttc gac act cgt gtt acg ctg cag gag   1315
Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg Val Thr Leu Gln Glu
390                 395                 400                 405

aag tca ctg gag ctt cca gct ctg cca acc acc acc att ggt tct ttc   1363
Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr Thr Ile Gly Ser Phe
                410                 415                 420

cca cag acc cca tcc att cgt tct gct cgc gct cgt ctg cgc aag gaa   1411
Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala Arg Leu Arg Lys Glu
            425                 430                 435
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tcc atc act ttg gag cag tac gaa gag gca atg cgc gaa gaa atc gat   1459
Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met Arg Glu Glu Ile Asp
        440                 445                 450

ctg gtc atc gcc aag cag gaa gaa ctt ggt ctt gat gtg ttg gtt cac   1507
Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu Asp Val Leu Val His
    455                 460                 465

ggt gag cca gag cgc aac gac atg gtt cag tac ttc tct gaa ctt ctc   1555
Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr Phe Ser Glu Leu Leu
470                 475                 480                 485

gac ggt ttc ctc tca acc gcc aac ggc tgg gtc caa agc tac ggc tcc   1603
Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val Gln Ser Tyr Gly Ser
                490                 495                 500

cgc tgt gtt cgt cct cca gtg ttg ttc gga aac gtt tcc cgc cca gcg   1651
Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn Val Ser Arg Pro Ala
            505                 510                 515

cca atg act gtc aag tgg ttc cag tac gca cag agc ctg acc cag aag   1699
Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln Ser Leu Thr Gln Lys
        520                 525                 530

cat gtc aag gga atg ctc acc ggt cca gtc acc atc ctt gca tgg tcc   1747
His Val Lys Gly Met Leu Thr Gly Pro Val Thr Ile Leu Ala Trp Ser
    535                 540                 545

ttc gtt cgc gat gat cag ccg ctg gct acc act gct gac cag gtt gca   1795
Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr Ala Asp Gln Val Ala
550                 555                 560                 565

ctg gca ctg cgc gat gaa att aac gat ctc atc gag gct ggc gcg aag   1843
Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile Glu Ala Gly Ala Lys
                570                 575                 580

atc atc cag gtg gat gag cct gcg att cgt gaa ctg ttg ccc gct acg   1891
Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu Leu Leu Pro Ala Thr
            585                 590                 595

aga cgt cga taagcctgcc tacctgcagt ggt                            1923
Arg Arg Arg
        600
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<213> Corynebacterium glutamicum

<400> 106

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Met Thr Ser Asn Phe Ser Ser Thr Val Ala Gly Leu Pro Arg Ile Gly
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Ala Lys Arg Glu Leu Lys Phe Ala Leu Glu Gly Tyr Trp Asn Gly Ser
             20                  25                  30

Ile Glu Gly Arg Glu Leu Ala Gln Thr Ala Arg Gln Leu Val Asn Thr
         35                  40                  45

Ala Ser Asp Ser Leu Ser Gly Leu Asp Ser Val Pro Phe Ala Gly Arg
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     50                  55                  60

Ser Tyr Tyr Asp Ala Met Leu Asp Thr Ala Ala Ile Leu Gly Val Leu
 65                  70                  75                  80

Pro Glu Arg Phe Asp Asp Ile Ala Asp His Glu Asn Asp Gly Leu Pro
                 85                  90                  95

Leu Trp Ile Asp Arg Tyr Phe Gly Ala Ala Arg Gly Thr Glu Thr Leu
            100                 105                 110

Pro Ala Gln Ala Met Thr Lys Trp Phe Asp Thr Asn Tyr His Tyr Leu
        115                 120                 125

Val Pro Glu Leu Ser Ala Asp Thr Arg Phe Val Leu Asp Ala Ser Ala
    130                 135                 140

Leu Ile Glu Asp Leu Arg Cys Gln Gln Val Arg Gly Val Asn Ala Arg
145                 150                 155                 160

Pro Val Leu Val Gly Pro Leu Thr Phe Leu Ser Leu Ala Arg Thr Thr
                165                 170                 175

Asp Gly Ser Asn Pro Leu Asp His Leu Pro Ala Leu Phe Glu Val Tyr
            180                 185                 190

Glu Arg Leu Ile Lys Ser Phe Asp Thr Glu Trp Val Gln Ile Asp Glu
        195                 200                 205

Pro Ala Leu Val Thr Asp Val Ala Pro Glu Val Leu Glu Gln Val Arg
    210                 215                 220

Ala Gly Tyr Thr Thr Leu Ala Lys Arg Asp Gly Val Phe Val Asn Thr
225                 230                 235                 240

Tyr Phe Gly Ser Gly Asp Gln Ala Leu Asn Thr Leu Ala Gly Ile Gly
                245                 250                 255

Leu Gly Ala Ile Gly Val Asp Leu Val Thr His Gly Val Thr Glu Leu
            260                 265                 270

Ala Ala Trp Lys Gly Glu Glu Leu Leu Val Ala Gly Ile Val Asp Gly
        275                 280                 285

Arg Asn Ile Trp Arg Thr Asp Leu Cys Ala Ala Leu Ala Ser Leu Lys
    290                 295                 300

Arg Leu Ala Ala Arg Gly Pro Ile Ala Val Ser Thr Ser Cys Ser Leu
305                 310                 315                 320

Leu His Val Pro Tyr Thr Leu Glu Ala Glu Asn Ile Glu Pro Glu Val
                325                 330                 335

Arg Asp Trp Leu Ala Phe Gly Ser Glu Lys Ile Thr Glu Val Lys Leu
            340                 345                 350

Leu Ala Asp Ala Leu Ala Gly Asn Ile Asp Ala Ala Ala Phe Asp Ala
        355                 360                 365

Ala Ser Ala Ala Ile Ala Ser Arg Arg Thr Ser Pro Arg Thr Ala Pro
    370                 375                 380
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Ile Thr Gln Glu Leu Pro Gly Arg Ser Arg Gly Ser Phe Asp Thr Arg
385 390 395 400

Val Thr Leu Gln Glu Lys Ser Leu Glu Leu Pro Ala Leu Pro Thr Thr
405 410 415

Thr Ile Gly Ser Phe Pro Gln Thr Pro Ser Ile Arg Ser Ala Arg Ala
420 425 430

Arg Leu Arg Lys Glu Ser Ile Thr Leu Glu Gln Tyr Glu Glu Ala Met
435 440 445

Arg Glu Glu Ile Asp Leu Val Ile Ala Lys Gln Glu Glu Leu Gly Leu
450 455 460

Asp Val Leu Val His Gly Glu Pro Glu Arg Asn Asp Met Val Gln Tyr
465 470 475 480

Phe Ser Glu Leu Leu Asp Gly Phe Leu Ser Thr Ala Asn Gly Trp Val
485 490 495

Gln Ser Tyr Gly Ser Arg Cys Val Arg Pro Pro Val Leu Phe Gly Asn
500 505 510

Val Ser Arg Pro Ala Pro Met Thr Val Lys Trp Phe Gln Tyr Ala Gln
515 520 525

Ser Leu Thr Gln Lys His Val Lys Gly Met Leu Thr Gly Pro Val Thr
530 535 540

Ile Leu Ala Trp Ser Phe Val Arg Asp Asp Gln Pro Leu Ala Thr Thr
545 550 555 560

Ala Asp Gln Val Ala Leu Ala Leu Arg Asp Glu Ile Asn Asp Leu Ile
565 570 575

Glu Ala Gly Ala Lys Ile Ile Gln Val Asp Glu Pro Ala Ile Arg Glu
580 585 590

Leu Leu Pro Ala Thr Arg Arg Arg
595 600

<210> 107
<211> 603
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(580)
<223> FRXA02086

<400> 107
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aacgatctca tcgaggctgg cgcgaagatc atccaggtgg atg agc ctg cga ttc 115
Met Ser Leu Arg Phe
1 5

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gtg aac tgt tgc ccg cta cga gac gtc gat aag cct gcc tac ctg cag   163
Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys Pro Ala Tyr Leu Gln
                10                  15                  20

tgg tcc gtg gac tcc ttc cgc ctg gcg act gcc ggc gca ccc gac gac   211
Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala Gly Ala Pro Asp Asp
            25                  30                  35

gtc caa atc cac acc cac atg tgc tac tcc gag ttc aac gaa gtg atc   259
Val Gln Ile His Thr His Met Cys Tyr Ser Glu Phe Asn Glu Val Ile
        40                  45                  50

tcc tcg gtc atc gcg ttg gat gcc gat gtc acc acc atc gaa gca gca   307
Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr Thr Ile Glu Ala Ala
    55                  60                  65

cgt tcc gac atg cag gtc ctc gct gct ctg aaa tct tcc ggc ttc gag   355
Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys Ser Ser Gly Phe Glu
70                  75                  80                  85

ctc ggc gtc gga cct ggt gtg tgg gat atc cac tcc ccg cgc gtt cct   403
Leu Gly Val Gly Pro Gly Val Trp Asp Ile His Ser Pro Arg Val Pro
                90                  95                  100

tcc gcg cag aaa gtg gac ggt ctc ctc gag gct gca ctg cag tcc gtg   451
Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala Ala Leu Gln Ser Val
            105                 110                 115

gat cct cgc cag ctg tgg gtc aac cca gac tgt ggt ctg aag acc cgt   499
Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys Gly Leu Lys Thr Arg
        120                 125                 130

gga tgg cca gaa gtg gaa gct tcc cta aag gtt ctc gtt gag tcc gct   547
Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val Leu Val Glu Ser Ala
    135                 140                 145

aag cag gct cgt gag aaa atc gga gca act atc taaattgggt taccgctagg 600
Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
150                 155                 160

aac                                                               603
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<210> 108
<211> 160
<212> PRT
<213> Corynebacterium glutamicum

<400> 108

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Met Ser Leu Arg Phe Val Asn Cys Cys Pro Leu Arg Asp Val Asp Lys
  1               5                  10                  15

Pro Ala Tyr Leu Gln Trp Ser Val Asp Ser Phe Arg Leu Ala Thr Ala
            20                  25                  30

Gly Ala Pro Asp Asp Val Gln Ile His Thr His Met Cys Tyr Ser Glu
        35                  40                  45

Phe Asn Glu Val Ile Ser Ser Val Ile Ala Leu Asp Ala Asp Val Thr
    50                  55                  60
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Thr Ile Glu Ala Ala Arg Ser Asp Met Gln Val Leu Ala Ala Leu Lys
65 70 75 80

Ser Ser Gly Phe Glu Leu Gly Val Gly Pro Gly Val Trp Asp Ile His
85 90 95

Ser Pro Arg Val Pro Ser Ala Gln Lys Val Asp Gly Leu Leu Glu Ala
100 105 110

Ala Leu Gln Ser Val Asp Pro Arg Gln Leu Trp Val Asn Pro Asp Cys
115 120 125

Gly Leu Lys Thr Arg Gly Trp Pro Glu Val Glu Ala Ser Leu Lys Val
130 135 140

Leu Val Glu Ser Ala Lys Gln Ala Arg Glu Lys Ile Gly Ala Thr Ile
145 150 155 160

<210> 109
<211> 1326
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1303)
<223> RXN02648

<400> 109
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gagtttgata ctttctttcg acttttagat tggatttca atg agc cag aac cgc 115
Met Ser Gln Asn Arg
1 5

atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
10 15 20

gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
25 30 35

ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
40 45 50

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
55 60 65

tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
70 75 80 85

ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
90 95 100

gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451

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Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
            105                 110                 115

cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct   499
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
        120                 125                 130

ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga   547
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
    135                 140                 145

cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg   595
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
150                 155                 160                 165

ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca   643
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
                170                 175                 180

gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac   691
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
            185                 190                 195

act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa   739
Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
        200                 205                 210

tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca ccg   787
Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala Pro
    215                 220                 225

gac ttg gca gaa gca tgg gat cag atc aac cca gag cca agc gtg aag   835
Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro Ser Val Lys
230                 235                 240                 245

gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc aac agt gca   883
Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile Asn Ser Ala
                250                 255                 260

gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc tgc tgg ggc   931
Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile Cys Trp Gly
            265                 270                 275

tct tgg cac gga cca cac gtc act gac atc cca ttc ggt gac atc att   979
Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly Asp Ile Ile
        280                 285                 290

ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc gaa ggc gca  1027
Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe Glu Gly Ala
    295                 300                 305

tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa aac aag ctt  1075
Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu Asn Lys Leu
310                 315                 320                 325

cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac tcc atc aac  1123
Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His Ser Ile Asn
                330                 335                 340

gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt cag ttc gcc  1171
Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val Gln Phe Ala
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            345                 350                 355

aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac tgt ggt ctg   1219
Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp Cys Gly Leu
        360                 365                 370

ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg gag tcc cta   1267
Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu Glu Ser Leu
    375                 380                 385

gta gag ggc gct cgc att gca tca aag gaa ctg ttc taagctagac       1313
Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
390                 395                 400

aacgagggtt gct                                                  1326


<210> 110
<211> 401
<212> PRT
<213> Corynebacterium glutamicum

<400> 110
Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
  1               5                  10                  15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
             20                  25                  30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
         35                  40                  45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
     50                  55                  60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
 65                  70                  75                  80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
                 85                  90                  95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
            100                 105                 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
        115                 120                 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn
    130                 135                 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
145                 150                 155                 160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
                165                 170                 175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
            180                 185                 190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
        195                 200                 205
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Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
210 215 220

Gln Leu Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro
225 230 235 240

Glu Pro Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp
245 250 255

Ala Ile Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu
260 265 270

His Ile Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro
275 280 285

Phe Gly Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe
290 295 300

Ser Phe Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp
305 310 315 320

Glu Glu Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val
325 330 335

Ser His Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg
340 345 350

Ile Val Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser
355 360 365

Thr Asp Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala
370 375 380

Lys Leu Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu
385 390 395 400

Phe

<210> 111
<211> 548
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (1)..(525)
<223> FRXA02648

<400> 111
gac gca ccg gac ttg gca gaa gca tgg gat cag atc aac cca gag cca 48
Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
1 5 10 15

agc gtg aag gat tac ttg gac tgg atc ggt aca cgc atc gat gcc atc 96
Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
20 25 30

aac agt gca gtg aag ggc ctt cca aag gaa cag acc cgc ctg cac atc 144

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Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
          35                  40                  45

tgc tgg ggc tct tgg cac gga cca cac gtc act gac atc cca ttc ggt   192
Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
     50                  55                  60

gac atc att ggt gag atc ctg cgc gca gag gtc ggt ggc ttc tcc ttc   240
Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
 65                  70                  75                  80

gaa ggc gca tct cct cgt cac gca cac gag tgg cgt gta tgg gaa gaa   288
Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
                 85                  90                  95

aac aag ctt cct gaa ggc tct gtt atc tac cct ggt gtt gtg tct cac   336
Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
            100                 105                 110

tcc atc aac gct gtg gag cac cca cgc ctg gtt gct gat cgt atc gtt   384
Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
        115                 120                 125

cag ttc gcc aag ctt gtt ggc cct gag aac gtc att gcg tcc act gac   432
Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
    130                 135                 140

tgt ggt ctg ggc gga cgt ctg cat tcc cag atc gca tgg gca aag ctg   480
Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
145                 150                 155                 160

gag tcc cta gta gag ggc gct cgc att gca tca aag gaa ctg ttc       525
Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
                165                 170                 175

taagctagac aacgagggtt gct                                        548


<210> 112
<211> 175
<212> PRT
<213> Corynebacterium glutamicum

<400> 112
Asp Ala Pro Asp Leu Ala Glu Ala Trp Asp Gln Ile Asn Pro Glu Pro
  1               5                  10                  15

Ser Val Lys Asp Tyr Leu Asp Trp Ile Gly Thr Arg Ile Asp Ala Ile
             20                  25                  30

Asn Ser Ala Val Lys Gly Leu Pro Lys Glu Gln Thr Arg Leu His Ile
         35                  40                  45

Cys Trp Gly Ser Trp His Gly Pro His Val Thr Asp Ile Pro Phe Gly
     50                  55                  60

Asp Ile Ile Gly Glu Ile Leu Arg Ala Glu Val Gly Gly Phe Ser Phe
 65                  70                  75                  80

Glu Gly Ala Ser Pro Arg His Ala His Glu Trp Arg Val Trp Glu Glu
                 85                  90                  95
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Asn Lys Leu Pro Glu Gly Ser Val Ile Tyr Pro Gly Val Val Ser His
100 105 110

Ser Ile Asn Ala Val Glu His Pro Arg Leu Val Ala Asp Arg Ile Val
115 120 125

Gln Phe Ala Lys Leu Val Gly Pro Glu Asn Val Ile Ala Ser Thr Asp
130 135 140

Cys Gly Leu Gly Gly Arg Leu His Ser Gln Ile Ala Trp Ala Lys Leu
145 150 155 160

Glu Ser Leu Val Glu Gly Ala Arg Ile Ala Ser Lys Glu Leu Phe
165 170 175

<210> 113
<211> 784
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(784)
<223> FRXA02658

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gagtttgata ctttctttcg acttttagat tggattttca atg agc cag aac cgc 115
Met Ser Gln Asn Arg
1 5

atc agg acc act cac gtt ggt tcc ttg ccc cgt acc cca gag cta ctt 163
Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg Thr Pro Glu Leu Leu
10 15 20

gat gca aac atc aag cgt tct aac ggt gag att ggg gag gag gaa ttc 211
Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile Gly Glu Glu Glu Phe
25 30 35

ttc cag att ctg cag tct tct gta gat gac gtg atc aag cgc cag gtt 259
Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val Ile Lys Arg Gln Val
40 45 50

gac ctg ggt atc gac atc ctt aac gag ggc gaa tac ggc cac gtc acc 307
Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu Tyr Gly His Val Thr
55 60 65

tcc ggt gca gtt gac ttc ggt gca tgg tgg aac tac tcc ttc acc cgc 355
Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn Tyr Ser Phe Thr Arg
70 75 80 85

ctg ggc gga ctg acc atg acc gat acc gac cgt tgg gca agc cag gaa 403
Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg Trp Ala Ser Gln Glu
90 95 100

gca gtg cgt tcc acc cct ggc aac atc gag ctg acc agc ttc tct gat 451
Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu Thr Ser Phe Ser Asp
105 110 115

cgt cgc gac cgc gca ttg ttc agc gaa gca tac gag gat cca gta tct 499
Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr Glu Asp Pro Val Ser
120 125 130

ggc atc ttc acc ggt cgc gct tct gtg ggc aac cca gag ttc acc gga 547
Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn Pro Glu Phe Thr Gly
135 140 145

cct att acc tac att ggc cag gaa gaa act cag acg gat gtt gat ctg 595
Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln Thr Asp Val Asp Leu
150 155 160 165

ctg aag aag ggc atg aac gca gcg gga gct acc gac ggc ttc gtt gca 643
Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr Asp Gly Phe Val Ala
170 175 180

gca cta tcc cca gga tct gca gct cga ttg acc aac aag ttc tac gac 691
Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr Asn Lys Phe Tyr Asp
185 190 195

act gat gaa gaa gtc gtc gca gca tgt gct gat gcg ctt tcc cag gaa 739
Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp Ala Leu Ser Gln Glu
200 205 210

tac aag atc atc acc gat gca ggt ctg acc gtt cag ctc gac gca 784
Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val Gln Leu Asp Ala
215 220 225

<210> 114
<211> 228
<212> PRT
<213> Corynebacterium glutamicum

<400> 114
Met Ser Gln Asn Arg Ile Arg Thr Thr His Val Gly Ser Leu Pro Arg
1 5 10 15

Thr Pro Glu Leu Leu Asp Ala Asn Ile Lys Arg Ser Asn Gly Glu Ile
20 25 30

Gly Glu Glu Glu Phe Phe Gln Ile Leu Gln Ser Ser Val Asp Asp Val
35 40 45

Ile Lys Arg Gln Val Asp Leu Gly Ile Asp Ile Leu Asn Glu Gly Glu
50 55 60

Tyr Gly His Val Thr Ser Gly Ala Val Asp Phe Gly Ala Trp Trp Asn
65 70 75 80

Tyr Ser Phe Thr Arg Leu Gly Gly Leu Thr Met Thr Asp Thr Asp Arg
85 90 95

Trp Ala Ser Gln Glu Ala Val Arg Ser Thr Pro Gly Asn Ile Glu Leu
100 105 110

Thr Ser Phe Ser Asp Arg Arg Asp Arg Ala Leu Phe Ser Glu Ala Tyr
115 120 125

Glu Asp Pro Val Ser Gly Ile Phe Thr Gly Arg Ala Ser Val Gly Asn

130 135 140

Pro Glu Phe Thr Gly Pro Ile Thr Tyr Ile Gly Gln Glu Glu Thr Gln
145 150 155 160

Thr Asp Val Asp Leu Leu Lys Lys Gly Met Asn Ala Ala Gly Ala Thr
165 170 175

Asp Gly Phe Val Ala Ala Leu Ser Pro Gly Ser Ala Ala Arg Leu Thr
180 185 190

Asn Lys Phe Tyr Asp Thr Asp Glu Glu Val Val Ala Ala Cys Ala Asp
195 200 205

Ala Leu Ser Gln Glu Tyr Lys Ile Ile Thr Asp Ala Gly Leu Thr Val
210 215 220

Gln Leu Asp Ala
225

<210> 115
<211> 408
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(385)
<223> RXC02238

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ctcttaacac tactgtccat atacttttga aaaggtgtca gtg acc aac gtg agc 115
Val Thr Asn Val Ser
1 5

aac gag acc aac gcc acc aag gcc gtc ttc gat ccg cca gtg ggc att 163
Asn Glu Thr Asn Ala Thr Lys Ala Val Phe Asp Pro Pro Val Gly Ile
10 15 20

acc gct cct ccg atc gat gaa ctg ctg gat aag gtc act tcc aag tac 211
Thr Ala Pro Pro Ile Asp Glu Leu Leu Asp Lys Val Thr Ser Lys Tyr
25 30 35

gcc ctc gtg atc ttc gca gcc aag cgt gcg cgc cag atc aac agc ttc 259
Ala Leu Val Ile Phe Ala Ala Lys Arg Ala Arg Gln Ile Asn Ser Phe
40 45 50

tac cat cag gca gat gag gga gta ttc gag ttc atc gga cca ttg gtt 307
Tyr His Gln Ala Asp Glu Gly Val Phe Glu Phe Ile Gly Pro Leu Val
55 60 65

act ccg cag cca ggc gaa aag cca ctt tct att gct ctg cgt gag atc 355
Thr Pro Gln Pro Gly Glu Lys Pro Leu Ser Ile Ala Leu Arg Glu Ile
70 75 80 85

aat gca ggt ctg ttg gac cac gag gaa ggt taaaagacct tataacttca 405
Asn Ala Gly Leu Leu Asp His Glu Glu Gly
90 95

cac 408

<210> 116
<211> 95
<212> PRT
<213> Corynebacterium glutamicum

<400> 116

Val	Thr	Asn	Val	Ser	Asn	Glu	Thr	Asn	Ala	Thr	Lys	Ala	Val	Phe	Asp
1				5				10				15			
Pro	Pro	Val	Gly	Ile	Thr	Ala	Pro	Pro	Ile	Asp	Glu	Leu	Leu	Asp	Lys
			20					25				30			
Val	Thr	Ser	Lys	Tyr	Ala	Leu	Val	Ile	Phe	Ala	Ala	Lys	Arg	Ala	Arg
		35					40					45			
Gln	Ile	Asn	Ser	Phe	Tyr	His	Gln	Ala	Asp	Glu	Gly	Val	Phe	Glu	Phe
	50					55					60				
Ile	Gly	Pro	Leu	Val	Thr	Pro	Gln	Pro	Gly	Glu	Lys	Pro	Leu	Ser	Ile
65					70					75					80
Ala	Leu	Arg	Glu	Ile	Asn	Ala	Gly	Leu	Leu	Asp	His	Glu	Glu	Gly	
				85					90					95	

<210> 117
<211> 1827
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1804)
<223> RXC00128

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cgttgatcgc tccagagaca ccgtgggaag gggagcagca gtg agt aaa att tcg 115
Val Ser Lys Ile Ser
1 5

acg aaa ctg aag gcc ctc acc gcg gtg ctg tct gtg acc act ctg gtg 163
Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser Val Thr Thr Leu Val
10 15 20

gct ggg tgt tcc acg ctt ccg cag aac acg gat ccg caa gtg ctg cgc 211
Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp Pro Gln Val Leu Arg
25 30 35

tca ttt tcc ggg tcc caa agc aca caa gag ata gca ggg ccg acc ccg 259
Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile Ala Gly Pro Thr Pro
40 45 50

aat caa gat ccg gat ttg ttg atc cgc ggc ttc ttc agc gca ggt gcg 307
Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe Phe Ser Ala Gly Ala
55 60 65

tat ccg act cag cag tat gaa gcg gcg aag gcg tat ctg acg gaa ggg 355
Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala Tyr Leu Thr Glu Gly
70 75 80 85

acg cgc agc acg tgg aat ccg gct gcg tcg act cgt att ttg gat cgc 403
Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr Arg Ile Leu Asp Arg
90 95 100

att gat ctg aac act ctg cca ggt tcg acg aat gcg gaa cga acg att 451
Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn Ala Glu Arg Thr Ile
105 110 115

gcg atc cgt gga acg cag gtc gga acg ttg ctc agc ggt ggc gtg tat 499
Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu Ser Gly Gly Val Tyr
120 125 130

cag ccg gag aat gcg gag ttt gaa gct gag atc acg atg cgt cgg gaa 547
Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile Thr Met Arg Arg Glu
135 140 145

gat ggg gag tgg cgt atc gat gct ttg ccg gac ggg att tta tta gag 595
Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp Gly Ile Leu Leu Glu
150 155 160 165

aga aac gat ctg cgg aac cat tac act ccg cac gat gtg tat ttc ttt 643
Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His Asp Val Tyr Phe Phe
170 175 180

gat cct tct ggc cag gtg ttg gtg ggg gat cgg cgt tgg ttg ttc aat 691
Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg Arg Trp Leu Phe Asn
185 190 195

gag tcg cag tcg atg tcc acg gtg ctg atg gcc ctt ctg gtt aat ggt 739
Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala Leu Leu Val Asn Gly
200 205 210

cct tcg ccg gca att tct cct ggt gtg gtc aat cag ctg tcc acg gat 787
Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn Gln Leu Ser Thr Asp
215 220 225

gcg tcg ttc gtg ggg ttc aat gat ggg gag tat cag ttc act ggt ttg 835
Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr Gln Phe Thr Gly Leu
230 235 240 245

gga aat ttg gat gat gat gcg cgt ttg cgt ttc gcc gcc cag gcc gtg 883
Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe Ala Ala Gln Ala Val
250 255 260

tgg acg ttg gcg cat gct gat gtc gca ggc ccc tac act ttg gtc gct 931
Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro Tyr Thr Leu Val Ala
265 270 275

gac ggc gcg ccg ttg ctg tcg gag ttc cca acg ctc acc acc gat gac 979
Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr Leu Thr Thr Asp Asp
280 285 290

ctc gcc gaa tac aac cca gag gct tac acc aac acg gtg tcc acg ttg 1027
Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn Thr Val Ser Thr Leu
295 300 305

ttt gcg ttg cag gat gga tcg ttg tcg agg gtc agt tcc ggc aat gtg 1075
Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val Ser Ser Gly Asn Val
310 315 320 325

agt cca cta cag ggc att tgg agc ggt gga gat atc gat tct gca gcg 1123
Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp Ile Asp Ser Ala Ala
330 335 340

att tcc tcc tcc gcc aat gtg gtg gca gcg gta cgc cac gaa aac aac 1171
Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val Arg His Glu Asn Asn
345 350 355

gag gca gtg ctt act gtt ggc tcc atg gaa ggc gtg act tca gat gcg 1219
Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly Val Thr Ser Asp Ala
360 365 370

ttg agg agt gaa acg atc act cgt ccc acc ttt gaa tac gcg tcg agt 1267
Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe Glu Tyr Ala Ser Ser
375 380 385

ggg ttg tgg gct gtg gtg gat ggg gag acg cct gtc cga gtc gca cga 1315
Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro Val Arg Val Ala Arg
390 395 400 405

tcg gca aca acc ggt gag ctc gtc cag acg gag gcg gag att gtg ctg 1363
Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu Ala Glu Ile Val Leu
410 415 420

cca agg gat gtg acg ggt ccg atc tct gaa ttc caa ctg tca cga act 1411
Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe Gln Leu Ser Arg Thr
425 430 435

ggg gtc cgg gcc gcc atg atc att gaa ggc aag gtg tac gtg ggc gtc 1459
Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys Val Tyr Val Gly Val
440 445 450

gta acg cgt cct ggt ccg ggc gag cgg cgc gtg aca aat atc acg gag 1507
Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val Thr Asn Ile Thr Glu
455 460 465

gtg gcg ccg agc ttg ggc gag gcg gcg ctg tcg atc aac tgg cgc cca 1555
Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser Ile Asn Trp Arg Pro
470 475 480 485

gac ggc att ttg ctt gtg ggc acg tca att cca gag acg ccg ctg tgg 1603
Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro Glu Thr Pro Leu Trp
490 495 500

cgc gtc gag cag gac gga tcg gcg att tcg tcg atg ccg agc ggg aat 1651
Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser Met Pro Ser Gly Asn
505 510 515

ctc agc gcg ccg gtg gtg gcg gtg gca agt tcc gcg acg acg gtc tac 1699
Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser Ala Thr Thr Val Tyr
520 525 530

gtc act gat tcg cat gcg atg ctt cag ctg ccg act gcc gat aat gat 1747
Val Thr Asp Ser His Ala Met Leu Gln Leu Pro Thr Ala Asp Asn Asp
535 540 545

att tgg cgc gag gtg ccc ggt ttg ctg ggc acg cgt gcg gcg ccg gtg 1795

Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr Arg Ala Ala Pro Val
550 555 560 565

gtt gcg tac tgatggagct gttcttcccg cgc 1827
Val Ala Tyr

<210> 118
<211> 568
<212> PRT
<213> Corynebacterium glutamicum

<400> 118
Val Ser Lys Ile Ser Thr Lys Leu Lys Ala Leu Thr Ala Val Leu Ser
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Val Thr Thr Leu Val Ala Gly Cys Ser Thr Leu Pro Gln Asn Thr Asp
20 25 30

Pro Gln Val Leu Arg Ser Phe Ser Gly Ser Gln Ser Thr Gln Glu Ile
35 40 45

Ala Gly Pro Thr Pro Asn Gln Asp Pro Asp Leu Leu Ile Arg Gly Phe
50 55 60

Phe Ser Ala Gly Ala Tyr Pro Thr Gln Gln Tyr Glu Ala Ala Lys Ala
65 70 75 80

Tyr Leu Thr Glu Gly Thr Arg Ser Thr Trp Asn Pro Ala Ala Ser Thr
85 90 95

Arg Ile Leu Asp Arg Ile Asp Leu Asn Thr Leu Pro Gly Ser Thr Asn
100 105 110

Ala Glu Arg Thr Ile Ala Ile Arg Gly Thr Gln Val Gly Thr Leu Leu
115 120 125

Ser Gly Gly Val Tyr Gln Pro Glu Asn Ala Glu Phe Glu Ala Glu Ile
130 135 140

Thr Met Arg Arg Glu Asp Gly Glu Trp Arg Ile Asp Ala Leu Pro Asp
145 150 155 160

Gly Ile Leu Leu Glu Arg Asn Asp Leu Arg Asn His Tyr Thr Pro His
165 170 175

Asp Val Tyr Phe Phe Asp Pro Ser Gly Gln Val Leu Val Gly Asp Arg
180 185 190

Arg Trp Leu Phe Asn Glu Ser Gln Ser Met Ser Thr Val Leu Met Ala
195 200 205

Leu Leu Val Asn Gly Pro Ser Pro Ala Ile Ser Pro Gly Val Val Asn
210 215 220

Gln Leu Ser Thr Asp Ala Ser Phe Val Gly Phe Asn Asp Gly Glu Tyr
225 230 235 240

Gln Phe Thr Gly Leu Gly Asn Leu Asp Asp Asp Ala Arg Leu Arg Phe
245 250 255

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Ala Ala Gln Ala Val Trp Thr Leu Ala His Ala Asp Val Ala Gly Pro
            260                 265                 270

Tyr Thr Leu Val Ala Asp Gly Ala Pro Leu Leu Ser Glu Phe Pro Thr
        275                 280                 285

Leu Thr Thr Asp Asp Leu Ala Glu Tyr Asn Pro Glu Ala Tyr Thr Asn
    290                 295                 300

Thr Val Ser Thr Leu Phe Ala Leu Gln Asp Gly Ser Leu Ser Arg Val
305                 310                 315                 320

Ser Ser Gly Asn Val Ser Pro Leu Gln Gly Ile Trp Ser Gly Gly Asp
                325                 330                 335

Ile Asp Ser Ala Ala Ile Ser Ser Ser Ala Asn Val Val Ala Ala Val
            340                 345                 350

Arg His Glu Asn Asn Glu Ala Val Leu Thr Val Gly Ser Met Glu Gly
        355                 360                 365

Val Thr Ser Asp Ala Leu Arg Ser Glu Thr Ile Thr Arg Pro Thr Phe
    370                 375                 380

Glu Tyr Ala Ser Ser Gly Leu Trp Ala Val Val Asp Gly Glu Thr Pro
385                 390                 395                 400

Val Arg Val Ala Arg Ser Ala Thr Thr Gly Glu Leu Val Gln Thr Glu
                405                 410                 415

Ala Glu Ile Val Leu Pro Arg Asp Val Thr Gly Pro Ile Ser Glu Phe
            420                 425                 430

Gln Leu Ser Arg Thr Gly Val Arg Ala Ala Met Ile Ile Glu Gly Lys
        435                 440                 445

Val Tyr Val Gly Val Val Thr Arg Pro Gly Pro Gly Glu Arg Arg Val
    450                 455                 460

Thr Asn Ile Thr Glu Val Ala Pro Ser Leu Gly Glu Ala Ala Leu Ser
465                 470                 475                 480

Ile Asn Trp Arg Pro Asp Gly Ile Leu Leu Val Gly Thr Ser Ile Pro
                485                 490                 495

Glu Thr Pro Leu Trp Arg Val Glu Gln Asp Gly Ser Ala Ile Ser Ser
            500                 505                 510

Met Pro Ser Gly Asn Leu Ser Ala Pro Val Val Ala Val Ala Ser Ser
        515                 520                 525

Ala Thr Thr Val Tyr Val Thr Asp Ser His Ala Met Leu Gln Leu Pro
    530                 535                 540

Thr Ala Asp Asn Asp Ile Trp Arg Glu Val Pro Gly Leu Leu Gly Thr
545                 550                 555                 560

Arg Ala Ala Pro Val Val Ala Tyr
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<210> 119
<211> 1344
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1321)
<223> RXA02240

<400> 119
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aagactattt attctcaact tcttcgaaag aagggtattt gtg gct cag cca acc 115
Val Ala Gln Pro Thr
1 5

gcc gtc cgt ttg ttc acc agt gaa tct gta act gag gga cat cca gac 163
Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr Glu Gly His Pro Asp
10 15 20

aaa ata tgt gat gct att tcc gat acc att ttg gac gcg ctg ctc gaa 211
Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu Asp Ala Leu Leu Glu
25 30 35

aaa gat ccg cag tcg cgc gtc gca gtg gaa act gtg gtc acc acc gga 259
Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr Val Val Thr Thr Gly
40 45 50

atc gtc cat gtt gtt ggc gag gtc cgt acc agc gct tac gta gag atc 307
Ile Val His Val Val Gly Glu Val Arg Thr Ser Ala Tyr Val Glu Ile
55 60 65

cct caa tta gtc cgc aac aag ctc atc gaa atc gga ttc aac tcc tct 355
Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile Gly Phe Asn Ser Ser
70 75 80 85

gag gtt gga ttc gac gga cgc acc tgt ggc gtc tca gta tcc atc ggt 403
Glu Val Gly Phe Asp Gly Arg Thr Cys Gly Val Ser Val Ser Ile Gly
90 95 100

gag cag tcc cag gaa atc gct gac ggc gtg gat aac tcc gac gaa gcc 451
Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp Asn Ser Asp Glu Ala
105 110 115

cgc acc aac ggc gac gtt gaa gaa gac gac cgc gca ggt gct ggc gac 499
Arg Thr Asn Gly Asp Val Glu Glu Asp Asp Arg Ala Gly Ala Gly Asp
120 125 130

cag ggc ctg atg ttc ggc tac gcc acc aac gaa acc gaa gag tac atg 547
Gln Gly Leu Met Phe Gly Tyr Ala Thr Asn Glu Thr Glu Glu Tyr Met
135 140 145

cct ctt cct atc gcg ttg gcg cac cga ctg tca cgt cgt ctg acc cag 595
Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ser Arg Arg Leu Thr Gln
150 155 160 165

gtt cgt aaa gag ggc atc gtt cct cac ctg cgt cca gac gga aaa acc 643
Val Arg Lys Glu Gly Ile Val Pro His Leu Arg Pro Asp Gly Lys Thr
170 175 180

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cag gtc acc ttc gca tac gat gcg caa gac cgc cct agc cac ctg gat    691
Gln Val Thr Phe Ala Tyr Asp Ala Gln Asp Arg Pro Ser His Leu Asp
            185                 190                 195

acc gtt gtc atc tcc acc cag cac gac cca gaa gtt gac cgt gca tgg    739
Thr Val Val Ile Ser Thr Gln His Asp Pro Glu Val Asp Arg Ala Trp
        200                 205                 210

ttg gaa acc caa ctg cgc gaa cac gtc att gat tgg gta atc aaa gac    787
Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp Trp Val Ile Lys Asp
    215                 220                 225

gca ggc att gag gat ctg gca acc ggt gag atc acc gtg ttg atc aac    835
Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile Thr Val Leu Ile Asn
230                 235                 240                 245

cct tca ggt tcc ttc att ctg ggt ggc ccc atg ggt gat gcg ggt ctg    883
Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met Gly Asp Ala Gly Leu
                250                 255                 260

acc ggc cgc aag atc atc gtg gat acc tac ggt ggc atg gct cgc cat    931
Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly Gly Met Ala Arg His
            265                 270                 275

ggt ggt gga gca ttc tcc ggt aag gat cca agc aag gtg gac cgc tct    979
Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser Lys Val Asp Arg Ser
        280                 285                 290

gct gca tac gcc atg cgt tgg gta gca aag aac atc gtg gca gca ggc    1027
Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn Ile Val Ala Ala Gly
    295                 300                 305

ctt gct gat cgc gct gaa gtt cag gtt gca tac gcc att gga cgc gca    1075
Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr Ala Ile Gly Arg Ala
310                 315                 320                 325

aag cca gtc gga ctt tac gtt gaa acc ttt gac acc aac aag gaa ggc    1123
Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp Thr Asn Lys Glu Gly
                330                 335                 340

ctg agc gac gag cag att cag gct gcc gtg ttg gag gtc ttt gac ctg    1171
Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu Glu Val Phe Asp Leu
            345                 350                 355

cgt cca gca gca att atc cgt gag ctt gat ctg ctt cgt ccg atc tac    1219
Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu Leu Arg Pro Ile Tyr
        360                 365                 370

gct gac act gct gcc tac ggc cac ttt ggt cgc act gat ttg gac ctt    1267
Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg Thr Asp Leu Asp Leu
    375                 380                 385

cct tgg gag gct atc gac cgc gtt gat gaa ctt cgc gca gcc ctc aag    1315
Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu Arg Ala Ala Leu Lys
390                 395                 400                 405

ttg gcc taaaaatctg atgtagtatc ttc                                  1344
Leu Ala
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<210> 120
<211> 407
<212> PRT
<213> Corynebacterium glutamicum

<400> 120
Val Ala Gln Pro Thr Ala Val Arg Leu Phe Thr Ser Glu Ser Val Thr
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Glu Gly His Pro Asp Lys Ile Cys Asp Ala Ile Ser Asp Thr Ile Leu
            20                  25                  30

Asp Ala Leu Leu Glu Lys Asp Pro Gln Ser Arg Val Ala Val Glu Thr
        35                  40                  45

Val Val Thr Thr Gly Ile Val His Val Val Gly Glu Val Arg Thr Ser
    50                  55                  60

Ala Tyr Val Glu Ile Pro Gln Leu Val Arg Asn Lys Leu Ile Glu Ile
65                  70                  75                  80

Gly Phe Asn Ser Ser Glu Val Gly Phe Asp Gly Arg Thr Cys Gly Val
                85                  90                  95

Ser Val Ser Ile Gly Glu Gln Ser Gln Glu Ile Ala Asp Gly Val Asp
            100                 105                 110

Asn Ser Asp Glu Ala Arg Thr Asn Gly Asp Val Glu Glu Asp Asp Arg
        115                 120                 125

Ala Gly Ala Gly Asp Gln Gly Leu Met Phe Gly Tyr Ala Thr Asn Glu
    130                 135                 140

Thr Glu Glu Tyr Met Pro Leu Pro Ile Ala Leu Ala His Arg Leu Ser
145                 150                 155                 160

Arg Arg Leu Thr Gln Val Arg Lys Glu Gly Ile Val Pro His Leu Arg
                165                 170                 175

Pro Asp Gly Lys Thr Gln Val Thr Phe Ala Tyr Asp Ala Gln Asp Arg
            180                 185                 190

Pro Ser His Leu Asp Thr Val Val Ile Ser Thr Gln His Asp Pro Glu
        195                 200                 205

Val Asp Arg Ala Trp Leu Glu Thr Gln Leu Arg Glu His Val Ile Asp
    210                 215                 220

Trp Val Ile Lys Asp Ala Gly Ile Glu Asp Leu Ala Thr Gly Glu Ile
225                 230                 235                 240

Thr Val Leu Ile Asn Pro Ser Gly Ser Phe Ile Leu Gly Gly Pro Met
                245                 250                 255

Gly Asp Ala Gly Leu Thr Gly Arg Lys Ile Ile Val Asp Thr Tyr Gly
            260                 265                 270

Gly Met Ala Arg His Gly Gly Gly Ala Phe Ser Gly Lys Asp Pro Ser
        275                 280                 285
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Lys Val Asp Arg Ser Ala Ala Tyr Ala Met Arg Trp Val Ala Lys Asn
290 295 300

Ile Val Ala Ala Gly Leu Ala Asp Arg Ala Glu Val Gln Val Ala Tyr
305 310 315 320

Ala Ile Gly Arg Ala Lys Pro Val Gly Leu Tyr Val Glu Thr Phe Asp
325 330 335

Thr Asn Lys Glu Gly Leu Ser Asp Glu Gln Ile Gln Ala Ala Val Leu
340 345 350

Glu Val Phe Asp Leu Arg Pro Ala Ala Ile Ile Arg Glu Leu Asp Leu
355 360 365

Leu Arg Pro Ile Tyr Ala Asp Thr Ala Ala Tyr Gly His Phe Gly Arg
370 375 380

Thr Asp Leu Asp Leu Pro Trp Glu Ala Ile Asp Arg Val Asp Glu Leu
385 390 395 400

Arg Ala Ala Leu Lys Leu Ala
405

<210> 121
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

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tcgggtatcc gcgctacactt aga 23

<210> 122
<211> 23
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 122
GGAAACCGGG GCATCGAAAC TTA 23

<210> 123
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 123
ggaaacagta tgaccatg 18

<210> 124
<211> 17
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 124
gtaaaacgac ggccagt 18

<210> 125
<211> 4334
<212> DNA
<213> Corynebacterium glutamicum

<400> 125
aaatcgcttg accattgcag gttggtttat gactgttgag ggagagactg gctcgtggcc 60

gacaatcaat gaagctatgt ctgaatttag cgtgtcacgt cagaccgtga atagagcact 120

taagtctgcg ggcattgaac ttccacgagg acgccgtaaa gcttcccagt aaatgtgcca 180

tctcgtaggc agaaaacggt tccccccgta ggggtctctc tcttggcctc ctttctaggt 240

cgggctgatt gctcttgaag ctctctaggg gggctcacac cataggcaga taacggttcc 300

ccaccggctc acctcgtaag cgcacaagga ctgctcccaa agatcttcaa agccactgcc 360

gcgactccgc ttcgcgaagc cttgccccgc ggaaatttcc tccaccgagt tcgtgcacac 420

ccctatgcca agcttctttc accctaaatt cgagagattg gattcttacc gtggaaattc 480

ttcgcaaaaa tcgtcccctg atcgcccttg cgacgttgct cgcggcggtg ccgctggttg 540

cgcttggctt gaccgacttg atcagcttgc atgcctgcag gtcgacggat ccccgggtgg 600

gaaagccacg ttgtgtctca aaatctctga tgttacattg cacaagataa aaatatatca 660

tcatgaacaa taaaactgtc tgcttacata aacagtaata caaggggtgt tatgagccat 720

attcaacggg aaacgtcttg ctcgaggccg cgattaaatt ccaacatgga tgctgattta 780

tatgggtata aatgggctcg cgataatgtc gggcaatcag gtgcgacaat ctatcgattg 840

tatgggaagc ccgatgcgcc agagttgttt ctgaaacatg gcaaaggtag cgttgccaat 900

gatgttacag atgagatggt cagactaaac tggctgacgg aatttatgcc tcttccgacc 960

atcaagcatt ttatccgtac tcctgatgat gcatggttac tcaccactgc gatccccggg 1020

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ctggcagtgt tcctgcgccg gttgcattcg attcctgttt gtaattgtcc ttttaacagc 1140

gatcgcgtat ttcgtctcgc tcaggcgcaa tcacgaatga ataacggttt ggttgatgcg 1200

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cacctgggca gagaaaattt ccagggcagc aagacccgcg acttcgccag cgcttggatc 3240

aaagacccgg acacgggaga aacacagccg aagttatacc gagttggttc aaaatcgctt 3300

gcccggtgcc agtatgttgc tctgacgcac gcgcagcacg cagccgtgct tgtcctggac 3360

attgatgtgc cgagccacca ggccggcggg aaaatcgagc acgtaaaccc cgaggtctac 3420

gcgattttgg agcgctgggc acgcctggaa aaagcgccag cttggatcgg cgtgaatcca 3480

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